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15-MAR-2002; 2002US-00098263.

US2003104410-A1. Homo sapiens.

05-JUN-2003

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ALIGNMENTS

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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                      Human microarray DNA oligonucleotide SEQ ID NO 60525.
ACI60534 standard; DNA; 25 BP
                                                         13-OCT-2003 (first entry)
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises motion at least one or more nucleic acids to at least two or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring corresponds are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms. CC of family members of a gene and a cross species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific acid probes is useful in in situ hybridisation, in Southern, Northern or dotter attached and previously sequenced. The sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by compared and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence of the moles of this patent can also be obtained in electronic format directly from USPTO at sequence. Itml
                                                                                                                                                                                                                                                                                                                                                                     in situ hybridization, in
to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 7 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              New array of nucleic acid probes, useful for
Southern, Northern or dot-blot hybridization
sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 60525; 9pp; English.
                                                                                                                                                                                    .6-MAR-2001; 2001US-0276759P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.0.
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                              (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                    WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                          Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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BP. AAA61982 standard; DNA; 20 AAA61982;

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Human MEXK5; mitogen-activated protein kinase kinase kinase 5; MEX kinase 5; MAP/BEK kinase 5; ASK1; pro-apoptotic; apoptosis signal-regulating kinase 1; programmed cell death; serine/threonine kinase; MAP kinase cascade; JNK/SAPK module; Jun N-terminal kinase/stress-activated protein kinase; p38 module; SEK1; transcription factor modulation; expression inhibition; antisense; Human MEKK5 phosphorothioate antisense oligonucleotide, SEQ ID NO:34. (first entry) 20-NOV-2000

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Sequences AAA61956-A61995 represent phosphorothioate antisense
cligonucleotides targetted to the human MEKK5 gene, which inhibit its
cligonucleotides targetted to the human MEKK5 gene, which inhibit its
cappression. The antisense oligonucleotides were designed to target
different regions of the human MEKK5 RNA, and were analysed for their
clifferent regions of the human MEKK5 RNA, and were analysed for their
effect on MEKK5 mRNA levels by quantitative real-time PCR. MEKK5 (also
controlled the member of transcription factors.

CC frown as MEKK5 is thought to play a critical role in the completion of apoptosis (programmed cell death) by interacting with other or cregulation of apoptosis (programmed cell death) by interacting with other controlling cascade and by phosphory-lating downstream targets such as MEKK3 and SEK1. MEKK5 also participates in another apoptosis-related as MIKK3 and SEK1. MEKK5 also participates in another apoptosis-related as MIKK3 and dimerisation of MEKK5 is induced by tumour necrosis factor—alpha (TNP-alpha), these processes being mediated by reactive oxygen captivation and dimerisation of MEKK5 is induced by reactive oxygen species. Thioredoxin is able to associate with MEKK5 and inhibit MEKK5 changes activity and hence MEKK5-dependent apoptosis. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associate with MEKK5 expression, such as inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense compounds useful for treating or preventing infection, inflammation or tumor formation by inhibiting expression of human MEKKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; light chain; complementarity determining region; CDR; beta-urease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. pylori beta-urease-binding antibody light chain CDR1 DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 13.8; DB 3; Length 20; 88.2%; Pred. No. 5.3e+03; ive 0; Mismatches 2; Indels
inflammation; wound healing disorder; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Col 39; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cowsert LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-464034/40.
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                                                                           Homo sapiens
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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAD) for their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of formation of a complex (C) between (I) and the corresponding antigen of (A). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (i) their native structure: or in at least some mammals, and have either: (i) their native structure: or infercted or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display or leacted or inferction by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter; specifically H. pylori, H. hepaticus, M. therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence encodes a fragment of a H. pylori beta-urease-binding antibody illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                         Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a fecal sample with two binding reagents for antigens that survive intestinal passage.
                                                                                                                                                                                                                       Lakner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.0%; Score 13.8; DB 3; Length 33; 88.2%; Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 BP; 10 A; 6 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                     Friedrichs U, Heppner P,
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 29; Page 23; 84pp; German.
                                                                                                                    98EP-00120517.
98EP-00120687.
                                                                                                                                                                                                                       Cullmann G,
                                                                                                                                                                                                                                                                                WPI; 2000-365747/31.
P-PSDB; AAB10016.
                                                                                                                                                                                 (CONN-) CONNEX GMBH
WO200026671-A1
                                                                                                                                       06-NOV-1998;
                                                                              29-OCT-1999;
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                                   11-MAY-2000.
                                                                                                                                                                                                                     Reiter C,
Ringeis A;
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Gaarde W;

ö H. pylori beta-urease derived antibody light chain CDR1 DNA #2. Indels 0; Mismatches 20 53 AAF88123 standard; DNA; 33 BP. 4 AACATCTATGTTTGGTT 13 AACATTAATGTTTGGTT 17-JUL-2001 (first entry) 15; Conservative Local Similarity AAF88123; Matches RESULT 4 AAF88123 음 à

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Gaps

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Gaps

; 0

Catalase; beta-urease; antibody; antigen; detection; infection; epitope; acid-resistant microorganism; complementarity determining region; CDR; feces; heavy chain; light chain; ds.

Unidentified.

WO200127612-A2

Haindl E;

Mueller H,

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This invention describes a novel method for detecting, in a mammal, infection by an acid-resistant microorganism (A) which comprises reacting a fecal sample with: (i) a receptor (R) such that a complex is formed with: (i) a receptor (R) such that a complex is formed with Ag, and the formation of a complex detected. R are complex is formed with Ag, and the formation of a complex detected. R are specific for an Ag which, after passage through the intestines, at least in some mammals, retains a native (or corresponding) structure against which the mammal produces antibodies (when immunized or infected with (A), or its extracts, lysates or derived proteins (or fragments) or synthetic peptides). The products of the invention have antibacterial activity. The method is used to diagnose infection by Helicobacter, Campylobacter or Mycobacterium, particularly H, pylori (most preferred), H, hepatica, C. jejuni and M. tuberculosis, and also to monitor the progress of treatment. Receptors, particularly antibodies, directed capanist Ag can be used therapeutically for treatment of infections. The method requires only one R to provide a reasonably secure diagnosis (although use of two R improves sensitivity), so is relatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geranylgeranyl diphosphate synthase; GGPP synthase; yew; cytostatic;
anticancer; Taxus; diterpene; paclitaxel; identification; plant;
Taxomyces andreanae; Penicillium raistrickii; microorganism; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inexpensive and more easily standardized. Also it is direct, non-
invasive, suitable for automation and may indicate the stage of an
infection. This sequence encodes a complementarity determining region
(CDR) from an antibody generated against a Helicobacter pylori antigen
(catalase or beta-urease) which is used to illustrate the method of the
                                                                                                                                                                                                                                                                                             Detecting infections by acid-resistant microorganisms, particularly diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%; Score 13.8; DB 4; Length 33; 88.2%; Pred. No. 5.46+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geranylgeranyl diphosphate synthase PCR primer SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33 BP; 10 A; 6 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                       (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
                                                                                                                                                         Cullmann G, Heppner P, Ringeis A,
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Page 18; 89pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                         31-MAR-2000; 2000EP-00107028.
10-MAY-2000; 2000EP-00110110.
16-MAR-2000; 2000EP-00105592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AACATCTATGTTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA13992 standard; DNA; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AACATTAATGTTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                              WPI; 2001-282087/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                             P-PSDB; AAB86064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taxus canadensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6043072-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2000.
                                                                                                                                                            Reiter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA13992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA13992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for detecting infection by an acid-resistant microorganism (A), in a mammal, using infection by an acid-resistant microorganism (A), in a mammal, using infection by an acid-resistant microorganism (A) in a mammal, such as Helicobacter, Campylobacter or Mycobacterium, particularly H. pylori (most preferred), H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple, inexpensive and non-invasive, and may indicate the stage of infection. A present in the method may include a filter to eliminate particles secure diagnosis, with specificity and selectivity improved by detecting several epitopes (of catalase) or different antigens (catalase) or different antigens (catalase and betaurease). The method can be automated. This sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting infections by acid-resistant microorganisms, particularly for diagnosing Helicobacter pylori, comprises immunochromatographic detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen; infection; acid-resistant microorganism; fecal; antibody; diagnosis; antibacterial; complementarity determining region; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementarity determining region (CDR) from an antibody raised against the H. pylori catalase or beta-urease antigen which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                      Schwartz G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori beta-urease derived antibody light chain CDR1 DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%; Score 13.8; DB 4; Length 33; 88.2%; Pred. No. 5.4e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                   Lakner M, Truee A, Dehnert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33 BP; 10 A; 6 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                           (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 30; Page 28; 90pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF88066 standard; DNA; 33 BP.
                                                                                                                          12-OCT-1999; 99EP-00120351.
16-MAR-2000; 2000EP-00105592.
31-MAR-2000; 2000EP-00107028.
10-MAY-2000; 2000EP-00110110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AACATCTATGTTTGGTT 20
                                                                        12-OCT-2000; 2000WO-EP010057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2000; 2000WO-EP010058.
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                                                                                                                                                                                                                                                                                                                   Reiter C, Cullmann G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of antigen in feces.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282086/29.
P-PSDB; AAB86096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                      19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-2001
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Query Match

Matches

AAF88066;

AAF88066

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Gaps

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The present sequence represents a PCR primer for a geranylgeranyl diphosphate (GGPP) synthase protein. GGPP synthase has cytostatic activity. A vector encoding GGPP synthase is useful in increasing GGPP synthase levels in a host cell preferably Taxus (Yew) cell and thereby facilitates production, isolation and purification of larger amounts of GGPP synthase in plants. GGPP synthase is useful in obtaining expression or enhanced expression of GGPP and other diterpenes, such as paclitaxel, useful as anticancer drugs. Isolated nucleic acids encoding GGPP synthase or hybridising with GGPP synthase encoding nucleic acids are used for identifying genes encoding GGPP synthase from microorganisms such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide-HOMO DNA-dependent 2-hydroxy acid dehydrogenase family protein 26.29 and encoding polynucleotide, used in diagnosis and treatment of e.g. malignant tumors, hemopathy, immunological diseases and
                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding geranylgeranyl diphosphate is useful for producing paclitaxel and other diterpenes that are useful as anticancer drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; DNA dependent 2-hydroxy acid dehydrogenase protein; enzyme;
cytostatic; virucidal; immunomodulatory; antiinflammatory; haemostatic;
malignant tumour; human immunodeficiency virus; HIV; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO 2-hydroxy acid dehydrogenase family protein 26.29 PCR primer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunological disease; gene therapy; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43 BP; 14 A; 6 C; 10 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taxomyces andreanae and Penicillium raistrickii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI
                                                                                                                                  (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Col 41; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AAGATCTATGTTTGATT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL99963 standard; DNA; 24 BP
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   98US-00187050
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88.2%;
                                                                   98US-00187050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88...
Best Local 15; Conservative
                                                                                                                                                                                                     Croteau RB, Hefner JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-340232/37.
                                                                                                                                                                                                                                                                         WPI; 2000-282526/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200232950-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2002
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05-NOV-1998;
                                                                   05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2002
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The invention relates to HOMO DNA-dependent 2-hydroxy acid dehydrogenase family protein 26.29 with cytostatic, virucidal, immunomodulatory, antinflammatory and haemostatic activity. The protein and encoding polynucleotide are used in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The polynucleotide is useful in gene therapy. The present sequence is that of a HOMO DNA-dependent 2-hydroxy acid dehydrogenase family protein 26.29 PCR primer, useful in examples of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for producing 1,3-propanediol from a carbon source, comprising culturing a recombinant microorganism having glycerol dehydratase and/or 1,3-propanediol dehydrogenase from Clostridium butyricum (see AAB73300, AAB80887 and AAB80889). The method of the present invention is useful for the production of 1,3-propanediol, which is useful as a stabiliser for lipases, amylases and proteases in wash liquids, as a protective emollient in liquid detergents for hand and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of 1,3-propanediol comprises culturing a recombinant microorganism expressing coenzyme B12-independent glycerol dehydratase.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dish washing, and as a monomer for producing polymers, especially polyesters, polyethers and polyurethanes. The present sequence is a promoter sequence, for glycerol dehydratase, which was used in the
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                                                                                                                                                                                                                                                        Score 13.6; DB 6; Length 24;
Pred. No. 6.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycerol dehydratase; 1,3-propanediol; enzyme stabiliser; polymer production; promoter; enzyme; ss.
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28 BP; 16 A; 2 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                       Sequence 24 BP; 13 A; 2 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                          0; Mismatches
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NAT SCI APPLIQUEES TOULOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycerol dehydratase promoter sequence.
              Example 2; Page 13; 37pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soucaille
                                                                                                                                                                                                                                                                                                                             1 AGTAACAICTAIGITIGGIT 20
                                                                                                                                                                                                                                                                                                                                                       22 AGTAACTTCTATATTTTGAT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 37; 69pp; French
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                                                                                                                                                                                                                                                        68.0%;
                                                                                                                                                                                                                                                                            80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
AAF77839/c
ID AAF77839 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Croux C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-247136/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
                                                                                                                                                                                      the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sarcabal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF77839;
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Best Local Similarity

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in manitoring gene expression levels by hybridisation to a DNA library, or an analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises completed acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring care expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid substitution to identify or detect the sequence or specific blot hybridisation to identify or detect the sequence or specific mattations of any gene, in mapping the 5' termin of mRNA molecules by the analysis or subclones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                      ..
         68.0%; Score 13.6; DB 4; Length 28; 80.0%; Pred. No. 6.7e+03; ive 0; Mismatches 4; Indels
                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Human microarray DNA oligonucleotide SEQ ID NO 17106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 9 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 17106; 9pp; English.
                                                                                             1 AGTAACATCTATGTTTGGTT 20
                                                                                                                                     26 AATAACATTTTTGTTTTT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                ACI17115 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                      (first entry)
Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                      13-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2003
                                                                                                                                                                                                                                                                                           ACI17115;
                                                                                                                                                                                                                              ACI17115/c
                                                                                                                                                                                                     RESULT
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DB 8; Length 25;

67.0%; Score 13.4;

Query Match

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Suggiments Analysis represent numbers which could be already and suggiments and suggiments and suggiments. The biallelic polymorphic markers. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in a method for determining polymorphic forms in an individual. The invention further provides computer-readable storage medium for storing data for access by an application programme being secured on a data processing system. Such a method comprises a data structure stored in the computer-readable storage medium, the data structure including information readident in a database used by the application programme and including records, each record comprising information identifying a polymorphism shown in the above sequences. The application programme and including records, each record comprising information identifying a polymorphism shown in the above sequences. The products and methods can be used for the presence of a disease phenotype or in formatics, paternity testing or genetic mapping of phenotypic traits. They can also be used for the production of transgenic animals. The nucleic acid segments can also be used in the manufacture of medicaments for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid segments containing polymorphic sites - used for, e.g. detecting a disease phenotype, in forensics, paternity testing or genetic mapping of phenotypic traits.
                                                                                                                                                                                                                                                                                                                                          Polymorphism; biallelic; paternity testing; forensic; genetic mapping; phenotypic typing; medicament; disease; marker; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAX06101-X06558 represent human DNA fragments which contain
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                 Indels
                                                                                                                                                                                                                                                                                                        Human biallelic polymorphic DNA fragment SGC34498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31 BP; 13 A; 6 C; 6 G; 5 T; 0 U; 1 Other;
93.3%; Pred. No. 8.3e+03;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment or prophylaxis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 28; 61pp; English.
                                                                                                                                                                                         AAX06450 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 AACACCTTTGTTTKGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AACATCTATGTTTGGTT
                                                                                                                                                                                                                                                                    (first entry)
                 14; Conservative
                                                       6 CATCTATGTTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-080963/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         W09858529-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipshutz RJ,
                                                                                                                                                                                                                                                                    31-MAR-1999
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                 Matches
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WO200253728-A2
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                              11-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence that encodes an enzymatically active BLM protein. This is used in the Single-Strand Conformation Polymorphism (SSCP) Analysis of the BLM gene. SSCP analysis helps in identifying the mutants in the BLM gene. Bloom's syndrome is diagnosed by detecting 2 mutated BLM genes or the absence of a wild-type BLM gene in a subject. Delivery of a functional BLM gene to bone marrow cells is used to treat or prevent the onset of Bloom's syndrome. Identification of the BLM gene and its products should assist in the development of therapeutic and diagnostic agents for cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM genes - for gene therapy with nucleic acid encoding active BLM protein to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                              cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This forward primer is used in the PCR amplification of the BLM gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida gene related tetracyclin promoter PCR primer SEQ ID NO 3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                           BLM; Bloom's syndrome; BS; mutant; probe; PCR primer; cancer; diagnosis; SSCP; Single-Strand Conformation Polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0%; Score 13.2; DB 2; Length 24; 83.3%; Pred. No. 1e+04; ive 0; Mismatches 3; Indels
                                                                                                                            Bloom's syndrome active BLM gene SSCP forward primer C1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 7 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

    for gene therapy with nucleic acid en
Bloom's syndrome and cancer in general.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 31; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          (NYBL-) NEW YORK BLOOD CENT INC.
                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGTAACATCTATGTTTGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                            Groden J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ29491 standard; DNA; 65 BP
                                                                                                                                                                                                                                                                                                                            96WO-US019046.
                                                                                                                                                                                                                                                                                                                                                           95US-00559303
                              AAT89524 standard; cDNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 acraccarcaarcarres
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                                                                                             (first entry)
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          German J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-289051/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans
                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                            WO9717979-A1
                                                                                                                                                                                                                                                                                                                           15-NOV-1996;
                                                                                             27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                           L5-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2003
                                                                                                                                                                                                                                                                                            22-MAY-1997
                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ29491;
                                                             AAT89524;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ellis N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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RESULT 11
AAT89524
XX
AAC AAT89
XX
DT 27-JA
XX
BLM;
XW BLM;
XW

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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by the selectable marker and modifying other allele by the combination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is sesential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the compound catabolism, biosynthetic, transporter transcriptional, compound catabolism, biosynthetic, transporter transcriptional, compound is useful for identifying a compound having the ability to inhibit growth or proliferation of cativity to inhibit growth or proliferation of cataboner each that of a primer used in the method of the invention. Note: The sequence is that of a primer used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis, antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptemer; HBV reverse transcriptase; Enhancer I region; viral replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65 BP; 17 A; 12 C; 14 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HBV hammerhead ribozyme substrate sequence #112.
                                                                                                                                                                                                                                                                                                                                                             Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
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                                                                                                                                                                                                                                                                                                                                                             Boone C,
                                                                                    29-DEC-2000; 2000US-0259128P.
                                                                                                                               20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
26-DEC-2001; 2001WO-US049486
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Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                             Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-566694/60
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RESULT 12

8 엄 Nucleic acid molecule, Hepatitis C virus, HCV, Hepatitis B virus, HBV; RNA stability; RNA expression; RNA synthesis, antisense; enzymetic nucleic acid, hammerhead riboxyme; DNAzyme, inozyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative, disease state, HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.

HBV inozyme substrate sequence #147.

(first entry)

24-SEP-2003

ACD51915;

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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, include antisense care nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV CONA. The nucleic acids may be used to modulate the expression of HBV canson and/or potential therapies directed against HBV, and compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, inozyme, zinzyme, DNAzyme or amberzyme sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
degenerative, disease state, HBV infection, HCV infection, cirrhosis, liver failure, hepatocellular carcinoma, hepatotropic, cytostatic, virucide, antiinflammatory, substrate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcswiggen J, Morrissey D, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 4 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 138; 387pp; English.
                                                                                                                                                                                                                      2001US-029677478.
2001US-0296876P.
2001US-0335059P.
                                                                                                                                                                                                                                                       24-OCT-2001; 2001US-0335059P. 05-DEC-2001; 2001US-0337055P.
                                                                                                                                                                      26-MAR-2002; 2002WO-US009187.
                                                                                                                                                                                                                                                                                                           RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macejak D,
Roberts E;
                                                                                                                                                                                                                                                                                                                                                         MCSWIGGEN J. MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-229207/22.
                                                                                                                                                                                                                                                                                                                           BLATT L.
MACEJAK D.
                                                                                                                                                                                                                                                                                                                                                                                          PAVCO P.
LEE P.
DRAPER K.
                                                                     Hepatitis B virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                               ROBERTS E.
                                                                                                    WO200281494-A1.
                                                                                                                                                                                                      26-MAR-2001;
08-JUN-2001;
                                                                                                                                                                                                                                       08-JUN-2001;
                                                                                                                                      17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blatt L, I
Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection.
                                                                                                                                                                                                                                                                                                           RIBO-)
                                                                                                                                                                                                                                                                                                                                                         (MCSW/)
                                                                                                                                                                                                                                                                                                                                                                                          (PAVC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                              ROBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                            DRAP/)
                                                                                                                                                                                                                                                                                                                           BLAT/)
                                                                                                                                                                                                                                                                                                                                          MACE/
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26-MAR-2001; 2001US-00817879. 08-JUN-2001; 2001US-00877478. 08-JUN-2001; 2001US-0296876P. 24-OCT-2001; 2001US-0335059F.

05-DEC-2001; 2001US-0337055P

RIBOZYME PHARM INC

MACEJAK D. MCSWIGGEN J. MORRISSEY D.

(BLAT/) (MACE/) (MCSW/) (RIBO-)

(MORR/) (PAVC/) (LEEP/) (DRAP/) (ROBE/)

26-MAR-2002; 2002WO-US009187

Hepatitis B virus.

WO200281494-A1.

17-OCT-2002.

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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes, inczymes, anozymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds, and/or potential therapies directed against HBV, and compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular cardinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences disclosed in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 5 A; 3 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 152; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection.
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Gaps

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64.0%; Score 12.8; DB 7; Length 17; 50.0%; Pred. No. 1.6e+04; ive 6; Mismatches 2; Indels

Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative

16

1 AGTAACATCTATGTTT

ઠે

AGGAACCUCUAUGUUU 16

Score 12.8; DB 7; Length 17; Pred. No. 1.6e+04;

64.0%; 50.0%;

Query Match Best Local Similarity

ACD51915 standard; RNA; 17 BP.

RESULT 14 ACD51915

ä ree

Pavco P,

Mcswiggen J, Morrissey D,

Roberts E;

Draper K,

Blatt L,

WPI; 2003-229207/22

Macejak D,

ROBERTS E. PAVCO P. LEE P. DRAPER K.

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, or monitoring gene expression levels by hybridisation to a DNA library, of at least one target sequence. The method of analysis comprises for incleic acid probes are specifically designed for analysis of at least one or more nucleic acids to at least two or more nucleic acids at least one or more nucleic acids to a least two or more content or a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, confamily members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises tag sequence. The array of nucleic acid further comprises of the sequence or specific or mutations of any gene, in mapping the 5' termini of mRNA molecules by containing segments of DNA that have been containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the concleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly compared in the microarray. Note: The sequence or sequence or sequence.
                                                                                                                                                                                                                                                        New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 60526; 9pp; English.
                                                                                           15-MAR-2002; 2002US-00098263.
                                                                                                                             16-MAR-2001; 2001US-0276759P.
                                                                                                                                                              (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                          WPI; 2003-567953/53.
                             US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Homo sapiens.
                                                                                                                                                                                             Mittmann MP;
                                                            05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACI01532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACI01532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duplex DNA (AAQ21864) (adapted from the L1 region of Human papilloma virus type 16) was used as a target to study the linear pre-amplification process. A probe set (QQ21865-8) was designed to hybridise to the target sequence for use in pre-amplification. The 3' end of probe 179.3 was haptenated with biotin-aminocaproyl NHS active ester. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Target-dependent prodn. of templates for ligase chain reaction -
increases sensitivity and detection of target from non-target contg.
                                                                                                                                                                                                                                                                              Templates; Human papilloma virus; ligase chain reaction; LCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 64.0%; Score 12.8; DB 2; Length 25; 1 Similarity 87.5%; Pred. No. 1.6e+04; 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                               Probe 179.3 DNA, to demonstrate controlled amplification.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human microarray DNA oligonucleotide SEQ ID NO 60526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 11 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
5
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimer GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 7; 20pp; English.
9
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                                                                                                                                    .867/c
AAQ21867 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                   91EP-00114541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-00575177
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                                16
                                                   2 AGGAACCUCUAUGUUU 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACI60535 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAACATCTATGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 GIAATATATATTTG
                                                                                                                                                                                                                23-JUN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-species comparison.
                               1 AGTAACATCTATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Backman KC, Carrino JJ,
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-073668/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ21862-78
                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-1992
                                                                                                                                                                                                                                                                                                                                                   EP473155-A
                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACI60535;
                                                                                                                                                                                 AAQ21867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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   Matches
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                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                              ;
                                          Score 12.8; DB 8; Length 25;
Pred. No. 1.6e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human microarray DNA oligonucleotide SEQ ID NO 1523.
Sequence 25 BP; 6 A; 4 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                  ACI01532 standard; DNA; 25 BP.
                                                                                                                                                   16
                                               / Match 64.0%;
Local Similarity 87.5%;
hes 14; Conservative
                                                                                                                                                                                             3 AGTAACATCGTTGTTT 18
                                                                                                                                                1 AGTAACATCTATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cross-species comparison.
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08-AUG-2002; 2002US-00215112. 08-AUG-2001; 2001US-0311040P.

US2003082596-A1

01-MAY-2003

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis compounds. The nucleic acid probes are specifically designed for analysis of genetic variation or in hybridisation. The nucleic acid probes are addence. The method of analysis comprises for hybridisating at least one or more nucleic acids to at least two or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the concleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotunelic acids further comprises a tag sequence or specific contactions of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening ONNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence and previously sequenced. The sequence presented is necessary from uncleic acid probes incorporated in the microarray. Note: The sequence and previously sequence or probe in sequence or specific for additional subclones containing segments of Note: The sequence or specific seconds for this patent can also be obtained in electronic format directly from used the nucleic acid probes incorporated in the sequence or specific seconds for this patent can also be obtained to the sequence or specific 
                                                                                                                                                                                                                                                                                                                                                                                                                         New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1523; 9pp; English.
                                                                                                                        15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                 16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                              (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-567953/53.
US2003104410-A1.
                                                                                                                                                                                                                                                                                                          Mittmann MP;
                                                            05-JUN-2003
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complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic useful in in situ hybridisations of a gene. The probes are also useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termin of mRNA molecules by primer extensions. The invention provides a large collection of nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. The sequence of the invention provides a large collection of nucleic acid sequences of Achsologica Achsologica and the invention provides a large collection of nucleic acid sequences.

New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.

WPI; 2003-576608/54.

Mittmann M;

(MITT/) MITTMANN M.

present invention relates to nucleic acid sequences that are

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Claim 1; SEQ ID NO 10981; 9pp; English.

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ACH57384 standard; DNA; 25 BP
                                                                                                                                               4 AACATCTATGTTTGGT 19
                                                                                                                                                                      AACTICTAIGTIIGCT 19
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                  14; Conservative
                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2003
                                                                                                                                                                                                                                                                                                                                                  ACH57384;
                                                                                                  Matches
                                                                                                                                                                                                                                                           RESULT 19
                                                                                                                                                                                                                                                                                  ACH57384
                                                                                                                                               8
                                                                                                                                                                                       g
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0
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene expression analysis, array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA target sequence #10981 useful in array for genetic analyses.
                                                                                                .<u>.</u>
                                            64.0%; Score 12.8; DB 8; Length 25; 87.5%; Pred. No. 1.6e+04; ive 0; Mismatches 2; Indels
Sequence 25 BP; 4 A; 4 C; 5 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                            ACH61845 standard; DNA; 25 BP.
                                                                                                                                        13
                                     Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                                  1 AACGICTATCTTTGGT 16
                                                                                                                                        4 AACATCTATGTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2003 (first entry)
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ACH61845;

RESULT 18 ACH61845

ਨੇ 셤 Unidentified

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The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; blrary screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.
                                                                                                                                                        :
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA target sequence #6520 useful in array for genetic analyses.
                                                                                                         64.0%; Score 12.8; DB 8; Length 25; 87.5%; Pred. No. 1.6e+04; ive 0; Mismatches 2; Indels
                                                              Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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Oat, Beta-amyrin synthase; triterpenoid, palatability, oxidosqualene cyclase; pathogen resistance; transgenic plant, fungal disease; sequencing primer; ss.
                                                                                                      Claim 1; SEQ ID NO 6520; 9pp; English
                                                                                                                                                                                                                                                                                                                                   AAS09822 standard; DNA; 30 BP
                                                                                                                                                                                                                                                                                            4 AACATCTATGTTTGGT 19
                       08-AUG-2002; 2002US-00215112.
                                                                                                                                                                                                                                                                         1 Similarity 87.5%;
14; Conservative
                                 08-AUG-2001; 2001US-0311040P
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                   WPI; 2003-576608/54.
                                                                                                                                                                                                                                                                           Local Similarity
                                             (MITT/) MITTMANN M.
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200146391-A2
US2003082596-A1
                                                                                                                                                                                                                                                                                                                                                           24-OCT-2001
           01-MAY-2003
                                                        Mittmann M;
                                                                                                                                                                                                                                                                                                                                                AAS09822;
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                        Matches
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The sequence represents a primer used to sequence nucleic acids encoding cat Beta-amyrin synthase (an oxidosqualene cyclase). Beta-amyrin is a cut interponding tresponsible for paltability to animals and resistance to pathogens and predators. The beta-amyrin synthase encoding nucleic acid is useful for producing a transgenic plant, by introducing a vector containing into a host cell, optionally causing or allowing crecombination between the vector and the host cell genome so as to transform the host cell, and regenerating a plant from the transformed creaming the presence of a nucleic acid in a sample and for influencing or affecting the quantity or quality of triterpenoid creaming the presence of a nucleic acid in a sample and for influencing or affecting the quantity or quality of triterpenoid creaming the presence of a nucleic acid in a sample and for influencing or altering resistance to a fungal pathogen e.g., an claim as altering resistance to a fungal pathogen e.g., an cascomycete having a sterol-containing membrane, optionally selected from ascomycete having a sterol-containing membrane, optionally selected from cascomycete having of the plant, by causing or allowing expression of the nutritional value, of the plant, following or allowing expression of the introducing the DNA into a cell or its ancestor. The DNA is also useful containing transcription from an antisense molecule in the plant, allowing transcription from an antisense molecule in the plant, allowing error allowing expression of the pracery of allowing transcription from an antisense molecule in the plant, allowing expression of the pracery of allowing transcription from an antisense molecule in the plant, allowing error e
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel beta-amyrin synthase encoding nucleic acids useful for influencing or affecting triterpene synthesis, and hence resistance to fungal pathogen, taste, palatability or nutritional value of plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription from the DNA, or its part such as to reduce beta-amyrin synthase expression by co-suppression, use of a nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Effector checkpoint protein kinase; Chk1; hyperproliferation; HIV; cancer; cytostatic; anti HIV; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

64.0%; Score 12.8; DB 4; Length 30;
Best Local Similarity 87.5%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 7 A; 8 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Chkl DNA amplifying primer chk6w.
                                                                                                                                                                                                                                                                                               Bryan GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 60; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF83283 standard; DNA; 34 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribozyme specific for the DNA
                                                                                                                                                                                                                                                                                               Haralampidis K,
                                                              20-DEC-2000; 2000WO-GB004908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                           16-AUG-2000; 2000GB-00020217.
                                                                                                                                   99GB-00030394
                                                                                                                                                                                                                             (PLAN-) PLANT BIOSCIENCE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ACATCCATGTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-418055/44.
                                                                                                                                22-DEC-1999;
                                                                                                                                                                                                                                                                                                      Osbourn AE,
28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF83283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF83283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to mutatic acts asymptomes that are comprises such as gene expression analysis. Each probe comprises you more consecutive nuclectides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, comprises you more consecutive nucleotides enjoyed in a maray comprising at least to distinct.

The probes may be used in an array comprising at least to distinct nucleic acid probes. The array is useful in monitoring gene expression nucleic acid probes. The array is useful in monitoring gene expression caseful for identifying family members of a gene. The probes are also useful in in situ hybridisations, in screening compounds. The probes are useful in in situ hybridisations, in screening compounds are also useful in in situ hybridisations, in screening containing segments of that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic Danes containing nay gene, and in may gene or detect specific mutations in any gene, and in captured and sequenced in symmetry to particular specific mutations in any gene, and in mapping the 5' termini of mrnA molecules by primer extensions. The complementary to particular sense with a wide range of analytical uses.

The invention provides a large collection of nucleic acid sequences of the invention are also useful as PCR primers. The sequence data for this patent was obtained in electronic format complemented and for this patent was obtained in electronic format the carget at sequences of the invention. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to nucleic acid sequences that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 6 A; 4 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oat Beta-amyrin synthase sequencing primer 64.
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Gaps

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EP1096014-A2. 02-MAY-2001

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                                                                                                                                                                                                         The invention relates to an isolated, soluble, catalytically active human effector checkpoint protein kinase (Chk1) polypeptide. Chk1 protein can be expressed by standard recombinant methodology. Chk1 is useful for screening for its inhibitors, used for treating hyperproliferative diseases, such as, HIV and cancer. The Chk1 DNA is useful for probes, primers, chemical intermediates, and in biological assays. Sequences AAF83283-290 represent PCR primers for amplifying the human Chk1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of
                                                                                                                                            Novel isolated, soluble, catalytically active human effector checkpoint protein kinase, useful for screening inhibitors of hChk1 kinase, for treating hyperproliferative disorders such as HIV and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.
                                                                                     Tempczyk-Russel A;
Lundgren K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer;
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida essential gene related knockout PCR primer SEQ ID NO 1712.
                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                 64.0%; Score 12.8; DB 4; Length 34; 87.5%; Pred. No. 1.6e+04; ive 0; Mismatches 2; Indels
                                                                                 n C, Luo C, Margosiak S, O'connor P, Tv
Sarup JC, Gaur S, Anderson MB, Deng Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL;
                                                                                                                                                                                                                                                                                             Sequence 34 BP; 6 A; 7 C; 7 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Виввеу Н,
                                                                                                                                                                                     Example 2; Page 15; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABZ27765 standard; DNA; 43 BP.
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          31-OCT-2000; 2000EP-00123738
                               99US-0162887P.
                                                                                                                                                                                                                                                                                                                                                           1 AGTAACATCTATGTTT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                         7 AGTACCATCTATCTTT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2001; 2001WO-US049486
                                                                                                                                                                                                                                                                                                                          87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2003 (first entry)
                                                             (AGOU-) AGOURON PHARM INC
                                                                                                                                                                                                                                                                                                                           Local Similarity 87.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) BLITRA PHARM INC.
                                                                                                                           WPI; 2001-302195/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida albicans
                                                                                   Kan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200253728-A2.
                              01-NOV-1999;
14-DEC-1999;
                                                                                                      Register J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2002.
                                                                                            Nguyen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ27765:
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                   Chen P,
                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 22
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion or replacement fragment with a heterologous promoter, so that expression of the sacond allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells in which both alleles modified are useful for identifying a gene that cells in which both alleles of a gene are modified. The diploid fungal contributes to the survival or growth of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus agent, an antifungal agent that inhibits the growth of a diploid fungus of and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, signal transduction, DNA replication and cell division attivity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a PCR construction into method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic map; haplotype; phenotype; polymorphic base; genotyping;
haplotyping; hybridisation; identification; characterisation; diagnosis;
single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome; biallelic marker; high density disequilibrium map;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                      Claim 76; SEQ ID NO 1712; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.0%; Score 12.8; DB 6; Length 43; 87.5%; Pred. No. 1.6e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43 BP; 24 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human map-related biallelic marker SEQ ID NO:1887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
replace(24,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 AGATCTATGTTTGTTT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0082614P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ67540 standard; DNA; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2001
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23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9954500-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-OCT-1999.
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Chumakov I;

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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the diffications responses to and side effects from the actually acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and and in the sequence Listing from the
                                                                                          Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 47 BP; 22 A; 5 C; 4 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                   Claim 1; Page 633; 2745pp; English.
Blumenfeld M,
                                                                                                                      map of the human genome
                                             WPI; 2000-013267/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
Cohen D,
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64.0%; Score 12.8; DB 3; Length 47; 87.5%; Pred. No. 1.7e+04; 2; Indels 0; Mismatches 5 ACATCTATGTTTGGTT 20 43 ACATTTATGTTTGTTT 28 Similarity 87.5%; 14, Conservative Query Match Best Local Similarity Matches g

ABL00484 standard; DNA; 51 BP ABL00484;

Human silent noncoding SNP oligonucleotide SEQ ID NO:475. (first entry) 05-MAR-2002

Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease; inflection; polymorphic protein; ds.

Homo sapiens

WO200138586-A2.

31-MAY-2001.

22-NOV-2000; 2000WO-US032311.

99US-0167383P 24-NOV-1999;

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-355949/37.

Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism

Claim 1; Page 391; 674pp; English

comperising one or more single nucleatide polymorphisms (SNPs). ABB56511

Comperising one or more single nucleatide polymorphisms (SNPs). ABB56511

Co ABB56903 represent human peptides encoded by some of the SNP

Co ilgonucleotides. The sequences from the present invention can have

condimicrobial activities. Nucleic acids, polypeptides, oligonucleotides

condimicrobial activities. Nucleic acids, polypeptides, oligonucleotides

condimicrobial activities. Nucleic acids, polypeptides, oligonucleotides

condimicrobial activities invention can be used for treating a

subject suffering from, at risk for, or suspected of, suffering from a

conject suffering from a fiseases, inflammation, cancer, diseases of

the nervous system, and infection by pathogenic microorganisms. The SNPs

care also useful for determining which forms of a characterised

conjectorium are present in individuals. The antibodies may be used in

conjectorium, quantitation and/or cellular or tissue localisation of a

conjectorium vithin appropriate physiological samples) ABL00010 to ABL01104 represent human nucleic acid oligonucleotides

Sequence 51 BP; 11 A; 12 C; 13 G; 15 T; 0 U; 0 Other;

Gaps ö Score 12.8; DB 5; Length 51; Pred. No. 1.7e+04; 0; Mismatches 2; Indels 64.0%; Query Match Best Local Similarity 87.5 Matches 14; Conservative

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셤 à

RESULT 25 AAZ44622,

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Gaps . 0 AAZ44622 standard; DNA; 58 BP

AAZ44622;

07-APR-2000 (first entry)

Newcastle disease virus LaSota primer BGL5F2.

Avian-paramyxovirus; infection; lentogenic; F protein; vaccine; respiratory disease; gastrointestinal disease; poultry pathogen; local immunity; primer; ss.

Newcastle disease virus.

WO9966045-A1.

23-DEC-1999.

99WO-NL000377. 17-JUN-1999; 98EP-00202054. 19-JUN-1998; (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.

Gielkens ALJ Koch G, Peeters BPH, De Leeuw OS,

WPI; 2000-106102/09.

New avian paramyxovirus cDNA, useful for production of vaccine against disease virus Newcastle

Disclosure; Page 33; 115pp; English.

This invention describes a novel avian-paramyxovirus cDNA (I) which comprises a nucleic acid sequence corresponding to the 5' terminal end of the genome of avian-paramyxovirus allowing the generation of an infectious copy of avian-paramyxovirus. The cell line is useful for the production of infectious lentogenic NDV (Newcastle Disease virus) without the addition of exogenous proteolytic activity. Also it is possible to generate a stable transfected cell line that expresses the wild-type F protein in the virus envelope therefore providing infectious particles, useful in the form of a vaccine, especially against respiratory and/or

analysis of S. cerevisiae YOL077C knock-out mutant

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Gaps

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The invention relates to genes in S. cerevisiae which are essential for germination and proliferation. The essential genes (EG) such as YDR141C, YDR091C, YOLOSCG, YOLOSAW and YOLO77C are used in a method for identifying potential antifungal compounds (CP). The method comprises overexpressing the EG cells, isolating a subset of genes induced of repressed by overexpression of EG and determining effect of Cp on down/up regulation of any subset of genes or contacting a protein encoded by EG with Cp and determining binding between them. Cp is identified as a potential antifungal Cp, if it downregulates a gene that is induced by coverxpression of EG or if it upregulates the gene that is repressed by coverxpression of EG or if it upregulates the protein encoded by coverage useful for identifying novel antifungal compounds for the method is useful for identifying novel antifungal compounds for treating fungal diseases and proliferative discorders in humans and nonthum mammals, including monkeys and other primates, dogs, cats.

Sequences AAFB23273-280 represents PCR primers for the construction and
gastrointestinal diseases. NDV can be easily cultured to very high titers in embryonated eggs. Mass culture of embryonated eggs is relatively cheap. NDV vaccines are relatively stable and can be simply administered by mass application methods e.g. drinking water or by spraying or by aerosol formation. The natural route of infection is by the respiratory and/or gastrointestinal fract which are also the major routes of infection of many other poultry pathogens. NDV can induce local immunity despite the presence of circulating maternal antibody. AAZ44527-Z44609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Germination; proliferation; essential gene; YDR141C; YDR091C; YOL026C;
YOL034W; YOL077C; antifungal; fungal disease; YOL022C; antisense therapy;
mutant; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying antifungal compounds for treating fungal and proliferative diseases, by using yeast genes essential for germination and proliferation as targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. cerevisiae YOL077C knock-out mutant constructing primer UPTAG.
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                             Length 58;
                                                                                                                                                                                                                                                                         Score 12.8; DB 3; Length 5 Pred. No. 1.7e+04; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                Sequence 58 BP; 21 A; 11 C; 11 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Fig 32; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ROSE-) ROSETTA INPHARMATICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                         5 ACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                   99US-00315793.
                                                                                                                                                                                                                                                                       ch 64.0%;
1 Similarity 87.5%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00315793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF83273 standard; DNA; 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae
                                                                                                                                                                                         strain LaSota genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-315575/33.
                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF83273;
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                            Microarray; probe; Mycobacterium; antibiotic-resistance; genotyping; ss.
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microarray for simultaneously genotyping Mycobacteria species, differentiating Mycobacterium tuberculosis strains and detecting antibiotic-resistant strains, comprises specific probes on a support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                         0
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                                                         64.0%; Score 12.8; DB 4; Length 74; 87.5%; Pred, No. 1.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%; Score 12.6; DB 7; Length 20; 78.9%; Pred. No. 2e+04; ive 0; Mismatches 4; Indels
                                                                                         Indels
                            Sequence 74 BP; 18 A; 20 C; 20 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                marinum - M ulcerans specific probe MAR-ULC-02,
                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 57; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GTAACATCTATGTTTGGTT 20
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                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2002; 2002WO-KR001885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2001; 2001KR-00062125.
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                                                                                                                                              23 ACATCCATCTTTGGTT 8
                                                                                                                                                                                                                        ACC73349 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SJHI-) SJ HIGHTECH CO LTD
                                                                                                                                                                                                                                                                                  15-JUL-2003 (first entry)
                                                                                                                   5 ACATCTATGTTTGGTT
                                                      Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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Best Local Similarity 78.9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jang H,
                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium marinum. Mycobacterium ulcerans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Park H,
                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003031654-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KIMC/) KIM C.
(PARK/) PARK H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2003,
                                                                                                                                                                                                                                                      ACC73349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX02618/c
ID AAX026
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Staphylococcus aureus.
                                                         WPI; 1999-083581/08.
     07-MAY-1999
                                       01-JUN-1998;
                                           04-JUN-1997;
                               EP892064-A2
                                   20-JAN-1999
                                                     Warren R,
                         Synthetic
 AAX02618;
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cc acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC perfect match perfect mismatch, antisense match or antisense mismatch. CC also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, cc in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. Each of the comprises in levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in is stu hybridisation, in Southern, Northern or dotuprobes is useful in in situ hybridisation, in Southern, Northern or dotuprobes is useful in in stu hybridisation, sequence or specific or mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones or inclair and problems of the sequence presented is one of the nucleic acid problems increment the sequence presented is one of the nucleic acid transfer in the sequence or presented is one of the sequence presented is one of the nucleic acid transfer in the problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its
                                                                                                                                                                            EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 12.6; DB 8; Length 25; 78.9%; Pred. No. 2e+04; rive 0; Mismatches 4; Indels
                                                                                                                 Human microarray DNA oligonucleotide SEQ ID NO 128010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 8 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 128010; 9pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2001; 2001US-0276759P.
                                                          (first entry)
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                                                                                                                                                                                                                                                   cross-species comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-567953/53.
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                                                                                                                                                                                                                                                                                                                                                                            US2003104410-A1
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mittmann MP;
                                                          14-0CT-2003
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ACK28029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes the isolation of a novel Staphylococcus aureus ATPase subunit of preprotein translocase (SecA). SecA polypeptides and polymerotein translocase (SecA). SecA polypeptides and underexpression of SecA protein by identifying mutations in the SecA gene, or determining SecA polypeptide or mRNA expression levels due to an infection of an organism with the SecA gene. They can diagnose the stage infection of an organism with the SecA gene. They can diagnose the stage and type of infection. SecA polypeptides can be used in treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance (agonist) SecA crivity. Diseases diagnosed, prevented or treated include bacterial infections, especially Staphylococcus aureus infections of the upper and lower respiratory tract (e.g. ottiss media, thyroiditis), cardiac (e.g. infective endocarditis), gastrointestinal (e.g. secretory diarrhoea, splenic abscess), CNS (e.g. crebral abscess), eye (e.g. conjunctivitis, keratitis, widney and urinary tract (e.g. toxic shock syndrome), skin (e.g. imperigo, wound infection), and bone and joint (e.g. septic arthritis, osteomyelitis). SecA polypeptides, polynucleotides and their (ant) agonists can prevent adhesion of bacteria to prevent bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Staphylococcus aureus ATPase subunit of preprotein translocase (SecA2) polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of Staphylococcus aureus infections, including toxic shock syndrome and splenic abscess.
                                                                                                                                                                                                                                                treatment; inhibit; antagonist; agonist; disease; bacterial; cardiac; respiratory tract; gastrointestinal; central nervous system; CNS; eye; kidney; urinary tract; skin; bone; joint; bacterial adhesion; wound; matrix proteins; body implant; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                         SecA2; ATPase subunit; preprotein translocase; diagnosis; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                  S. aureus SecA2 PCR primer #1.
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                                                                                                    (first entry)
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2 GTAACATCTATGTTTGGTT 20

Query Match

Local

Matches

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GTAACATCTAGTTTATGTT

ACK28029 standard; DNA; 25 BP

RESULT 29
ACK28029/c
ID ACK28

ACI29919 standard; DNA; 25

ACI29919

RESULT 30 ACI29919/c ID ACI299 XX AC ACI299

ss; probe; expressed sequence tag; microarray; gene expression; ic variation; biallelic marker; polymorphism; human;

cross-species comparison.

JS2003104410-A1. Homo sapiens.

05-JUN-2003

genetic variation;

15-MAR-2002; 2002US-00098263. 16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

Mittmann MP;

WPI; 2003-567953/53.

Human microarray DNA oligonucleotide SEQ ID NO 36372.

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis. The array is used in analysis. The array is used in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparises, acid the conclet acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific conclets as useful in in situ hybridisation, in Southern, Northern or dottores is useful in in situ hybridisation, in Southern, Northern or dottores are attached to a solid suppond the 5' termini of many molecules by compared to a solid suppond the 5' termini of many molecules by compared to a solid suppond the 5' termini of many molecules by compared to a solid suppond the 5' termini of many and the sequence or specific.

The follow of the sequence or specific acid for additional subclones containing segments of but that have been the sequence or specific acid for additional subclones containing segments of but that have been sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                          EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                               Human microarray DNA oligonucleotide SEQ ID NO 29910.
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0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                            15-MAR-2002; 2002US-00098263.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-567953/53.
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                                                                                                                                                                                                          sapiens.
  13-OCT-2003
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 36372; 9pp; English.

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of the probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring confamily members of a gene and a cross-species comparison. Each of the nucleic acids further comprises species comparison. Each of the concleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific or probes is useful in in situ hybridisation, in Southern, Northern or dotuposes is useful in in situ hybridisation, in Southern, Northern or dotuposes is useful in in situ hybridisation, in Southern, Northern or dotupose primer extensions or in screening cDNA or genomic libraries or subclones cortain subclones containing segments of DNA that have been conformed and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence of the nucleic acid probes incorporated in the microarray. Note: The sequence of the mucleic acid probes incorporated in the sequence presented is one of the conditional sequence or sequence presented is one of the sequence or securing or sequence or sequence or sequence or sequence or sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score Larry,
Pred. No. 2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human microarray DNA oligonucleotide SEQ ID NO 65195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 9 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGTAACATCTATGTTTGGT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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BP.

ACI36381 standard; DNA; 25

RESULT 31

(first entry)

13-OCT-2003

ACI36381;

ACI36381/c 1D ACI363 XX XC ACI363 XC ACI363 DT 13-OCT

cross-species comparison.

US2003104410-A1. Homo sapiens.

05-JUN-2003

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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                                                                                            Claim 1; SEQ ID NO 65195; 9pp; English.
                                                                               15-MAR-2002; 2002US-00098263.
                                                                                              16-MAR-2001; 2001US-0276759P.
                                                                                                              (AFFY-) AFFYMETRIX INC
                                                 US2003104410-A1
                                  Homo sapiens.
                                                                05-JUN-2003.
                                                                                                                              Mittmann MP;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Compounds a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific additional subclones containing segments of DNA that have been to prime extensions of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been contained and previously sequenced. The sequence date for this patent can also be obtained in electronic format directly from USPTO at sequence thum
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Pred. No. 2e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 4 A; 4 C; 8 G; 9 T; 0 U; 0 Other;
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0
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Local Similarity 78.9%;
les 15; Conservative (
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring can expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid by hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening DNA or genomic libraries or subclones for additional subclones containing segments of bush that have been isolated and previously sequenced. The sequence presented is one of the

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

LS-MAR-2002; 2002US-00098263. 16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

WPI; 2003-567953/53.

Mittmann MP;

Claim 1; SEQ ID NO 100102; 9pp; English

isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html

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13-OCT-2003
                                                                                                                                AC127083;
Matches
                                                                                 RESULT 34
                       à
                                             셤
                                                 GTAACATCTATGTTTGGTT 20
                                                                       Gradcaggradgrircgrr 20
                                                                                                                                    BP
                                                                                                                                    ACK00121 standard; DNA; 25
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                   14-OCT-2003
                                                                                                                                                            ACK00121;
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RESULT 33

8

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;

Human microarray DNA oligonucleotide SEQ ID NO 100102.

ACK00121 ID ACK XX AC ACK XX DT 14-6 XX XX DE Hum DE Hum KW EST KW Gen

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                                                                                                                                                                                                                                                                                                             63.0%; Score 12.6; DB 8; Length 25; 78.9%; Pred. No. 2e+04; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Human microarray DNA oligonucleotide SEQ ID NO 27074.
                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 5 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                AGTACCATCTACGTTCCGT 21
                                                                                                                                                                                                                                                                                                                                                                                   ACI27083 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                Query Match
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its component match, perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, cC in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises comparises and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid content of dentify or detect the sequence or specific or nucleic acids further or identify or detect the sequence or specific or probes is useful in in situ hybridisation, in Southern, Northern or detect the additional subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence or appendence or an also be obtained in electronic format directly from treath or an also be obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                         New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 7 A; 3 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.goc/seguence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 27074; 9pp; English.
                                                                                                                                                   L5-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                      16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                      (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-567953/53,
                                                US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USPTO at
Homo sapiens.
                                                                                                   05-JUN-2003.
                                                                                                                                                                                                                                                                                                         Mittmann MP;
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

WPI; 2003-567953/53.

Mittmann MP;

15-MAR-2002; 2002US-00098263.

US2003104410-A1

05-JUN-2003

Claim 1; SEQ ID NO 35736; 9pp; English.

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1 AGTAACATCTATGTTTGGT 19
                                                                                                            24 AGTAACTICAATGICIGII 6
                                                                                                                                                                                                ACI25132 standard; DNA; 25 BP
                    78.9%;
     63.0%;
                                                                                                                                                                                                                                                                      (first entry)
Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                      13-OCT-2003
                                                                                                                                                                                                                                   ACI25132;
                                                                                                                                                               RESULT 36
ACI25132/c
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                                                                       Gaps
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                                    DB 8; Length 25;
                                                   Pred. No. 2e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                    Human microarray DNA oligonucleotide SEQ ID NO 35736.
                                  63.0%; Score 12.6;
                                                                                                      1 AGTAACATCTATGTTTGGT 19
                                                                                                                                     1 AGTAATAGATATGTTTCGT 19
                                                                                                                                                                                                                            ACI35745 standard; DNA; 25 BP.
                                                 78.98;
                                                                                                                                                                                                                                                                                               (first entry)
                                                                   15; Conservative
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Local Similarity

Matches

Query Match

cross-species comparison.

13-OCT-2003 ACI35745;

ACI35745/c

RESULT 35

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Homo sapiens,

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its C acid probes including one of 2,018,500 fully defined sequences, or its C Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dottor hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' terminal of mRNA molecules by comparisons of any gene, in mapping the 5' terminal of DNA that have been containing segments of DNA that have been sololated and previously sequenced. The sequence presented is one of the concleic acid probes incorporated in the microarray. Note: The sequence containing sequence the sequence and probes incorporated in the microarray. Note: The sequence of the form USPPO at sequence of the concleic acid probes incorporated in the microarray. The sequence
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microarray DNA oligonucleotide SEQ ID NO 25123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003104410-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in manlysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises in hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tay sequence. The array of nucleic acid further comprises a tay sequence. The array of nucleic acid further comprises a tay sequence. The array of nucleic acid further comprises a tay sequence. The array of nucleic acid for any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the form of t
                                                                                                                                                                                                                                                                                                                                                                                   New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 25123; 9pp; English.
                                                                                                                             16-MAR-2001; 2001US-0276759P.
                                                            15-MAR-2002; 2002US-00098263
                                                                                                                                                                                         (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                          WPI; 2003-567953/53.
05-JUN-2003
                                                                                                                                                                                                                                                             Mittmann MP
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Gaps
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63.0%; Score 12.6; DB 8; Length 25; 78.9%; Pred. No. 2e+04; ive 0; Mismatches 4; Indels
                                 15; Conservative
                Best Local Similarity
   Query Match
                               Matches
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2 GTAACATCTATGTTTGGTT 20
                       BP.
      GAAGGATCTATCTTTGGTT
                       ACI35606 standard; DNA; 25
                              ACI35606;
                ð
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Human microarray DNA oligonucleotide SEQ ID NO 35597. (first entry) 13-0CT-2003

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison

Homo sapiens

JS2003104410-A1

05-JUN-2003

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and at least two or more nucleic acid probes and acted to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of agene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-probes is useful in in situ hybridisation, in Southern, Northern or dot-probes is useful in a mapping the 5' termin of many molecules by prime expressions or in screening conk or genenic of any gene, in mapping the 5' termin of many have been a party for the companies of my have been any accounted to the companies of my have been any accounted to the companies of my have been any sone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for this patent can also be obtained in electronic format directly
                                                                                                                                                                                                                                                                                   New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 35597; 9pp; English.
                                                      16-MAR-2001; 2001US-0276759P
15-MAR-2002; 2002US-00098263
                                                                                                               (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                               WPI; 2003-567953/53
                                                                                                                                                                         Mittmann MP;
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Gaps : 0 Score 12.6; DB 8; Length 25; Pred. No. 2e+04; 0; Mismatches 4; Indels Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other; Query Match 63.0%; Best Local Similarity 78.9%; Matches 15; Conservative (

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GTAACATCTATGTTTGGTT 20 Graacaggragerricerr 19 N

> q ₽

Primer for ASTH1 polmorphic microsatellite marker. AAZ18573/c ID AAZ18573 standard; DNA; 27 19-OCT-1999 (first entry) AAZ18573; RESULT 38

ASTH1; asthma; human; chromosome 11p; ASTH11; ASTH1J; genetic locus; ss; therapeutic; immunogen; polymorphism; PCR primer; microsatellite marker. Synthetic. Homo sapiens

98WO-US001260. 21-JAN-1998; 29-JUL-1999.

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                                                                                                                                                                                                                                          mapped to human chromosome 11p. ASTHII and ASTHIIJ are genes present within the locus, located close to each other on human chromosome 11p, and have similar patterns of expression, and common sequence motifs. The ASTHI genes and fragments, encoded protein, genomic regulatory regions and anti-ASTHI antibodies are useful in the identification of individuals predisposed to development of asthma, and for the modulation of gene activity in vivo for prophylactic and therapeutic purposes. The ASTHI protein is useful as an immunogen to raise specific antibodies, in drug screening for compositions that mimic or modulate ASTHI activity or expression, including altered forms of ASTHI protein, and as a therapeutic. Sequences AAZI8510-2186311 represent PCR primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASTH1 polymorphic microsatellite marker AFMA154ZD1 primer, SEQ ID NO:223.
                                                                                                                                              Mammalian asthma related genes, useful for diagnosis of a predisposition to development of asthma.
                                                                                                                                                                                                                            The invention identifies a genetic locus ASTH1, associated with asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody; drug screening; prophylaxis; therapy, diagnosis; polymorphic microsatellite marker flanking sequence; batched analysis of genotypes; BAGs; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                 Carey AH, Galvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 12.6; DB 2; Length 27; 78.9%; Pred. No. 2e+04; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphic microsatellite markers in the ASTH1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buckler A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 BP; 5 A; 6 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardon L,
                                                               Cardon L,
                                                                                                                                                                                              Disclosure; Page 50; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 AGTAACATCTCAGCCTGGT 9
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                                                               Buckler A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
98WO-US001260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA80480 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 78,9
                              (AXYS-) AXYS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller A,
                                                             Brooks-Wilson AR, I
Miller A, North M;
                                                                                                             WPI; 1999-479058/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brooks-Wilson AR,
21-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA80480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH1 and ASTH1J genes, which chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes are oriented in opposite of APTH conditions with the ASTH1 and ASTH1J are novel members of expression and common sequence motifs. They are both expressed in trached, lung and common sequence motifs. They are both expressed in trached, lung and common sequence motifs. They are both expressed in trached, lung and common sequence motifs. They are both expressed in trached, lung and common sequence motifs. They are both expressed in trached, transcription factors, which have been implicated in the common sequence motifs. They are both expressed in trached, attentively spliced. Alternative splicing of ASTH1 mans a no effect on the open reading frame of ASTH1J and ASTH1I mans an offect on the open reading frame of ASTH1J and alternative splicing of ASTH1I transcripts results in 3 different ASTH1I inscripts a precision of a stanscripts are useful as dagnostics to identifying ASTH1 related genes, for identifying expression of the gene in a biological specimen, and for generating geneticinally modified non-human animals or site specific gene (modifications that mimic or modulate activity or expression of ASTH1I compositions that mimic or modulate activity or expression of ASTH1I compositions that mimic or modulate activity or expression of ASTH1I compositions that mimic or modulate activity or expression of ASTH1I compositions that mimic or modulate activity or expression of ASTH1I compositions that mimic or modulate activity or expression of ASTH1I compositions that mimic or modulate activity or expression of ASTH1I compositions that mimic or modulate activity or expression of ASTH1I and as a theorem of activity in vivo for compositions that mimic or modulate activity or expression of ASTH1I and a therapeutic purposes the intract ASTH1I and a therapeutic purposes the intract ASTH1I and therapeutic purposes the intra
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               New nucleic acids other than naturally occurring chromosomes encoding ASTH1 protein, for e.g. screening compositions that modulate expression or function of ASTH1 proteins or as diagnostics for genetic predisposition to asthma.
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antiparkinsonian; antilipaemic; gene therapy; metabolic disorder;
diabetes; obesity; infection; cachearis cancer; PCR; primer;
neurodegenerative disorder; Alzabaimer's disease; Parkinson's disease;
immune disorder; haematopoletic disorder; dyslipidaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.0%; Score 12.6; DB 3; Length 27; 78.9%; Pred. No. 2e+04; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 5 A; 6 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        batched analysis of genotypes (BAGs)
                                                                                                                                            Example; Col 31-32; 131pp; English.
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ID ACC72239 standard; DNA; 27 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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WO2003029423-A2.

WPI; 2000-505109/45.

(first entry)

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Homogeneous neurotrophic factor for treating neuro-degenerative diseases, e.g. Parkinsonism - comprise specified polypeptide sequence lacking micro-heterogeneity associated with a related native sequence factor.
                                                    quence of PCR primer which corresp, to the sense strand for AAs 76-87 ciliary neurotrophic factor (CNTF).
                                                                                                                       Neurotrophic factor; neuro-degenerative disease; therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                     Higaki JN, Tischer EG,
                                                                                                                                                                                                                                                                                                                                                                             (SCIO-) SCIOS NOVA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-093724/11
                                                                                                                                                                                                                                                                                           21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                    23-AUG-1991;
                                                                                                                                                                                                          WO9303758-A1
25-MAR-2003
03-JUL-1993
                                                                                                                                                                                                                                                   04-MAR-1993.
                                                               Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                   Synthetic
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ID ABK9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel human NOV proteins and their coding sequences (ACC72075-ACC72181 and ABRS8863-ABRS8465). The NOV proteins are useful in manufacturing a medicament for treating a syndrome associated with a human disease. The NOV proteins and coding sequences may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoletic disorders and various dyslipidaemias. The present sequence is a PCR primer, used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVX polypeptides and nucleic acids useful for diagnosing, preventing treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E; Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W; Kekuda R, Leach MD, Li L, Miller CE, Patturajan M, Rieger DK; Rothenberg ME, Shinkers RA, Smithson G, Spytek KA, Taupier RJ; Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
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                                                                                                    02-OCT-2001; 2001US-0326483P.

05-OCT-2001; 2001US-03237342P.

09-OCT-2001; 2001US-0328029P.

09-OCT-2001; 2001US-0328034P.

09-OCT-2001; 2001US-0328056P.

12-OCT-2001; 2001US-0328149P.

15-OCT-2001; 2001US-0328414P.

17-OCT-2001; 2001US-0328414P.

17-OCT-2001; 2001US-0339266P.

24-OCT-2001; 2001US-0339266P.

24-OCT-2001; 2001US-0343629P.
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                                                                                                                                                                                                                                                                                                                                    2001US-0343629P.
2001US-0349575P.
2001US-0346357P.
2002US-0371972P.
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17-MAY-2002; 2002US-0381635P.
29-MAY-2002; 2002US-0383830P.
                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2002; 2002US-0371980P.
17-APR-2002; 2002US-0373261P.
                                                                 02-OCT-2002; 2002WO-US031358
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15; Conservative
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                              29-OCT-2001;
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                          10-APR-2003
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Thompson SA;

Cordell B,

92WO-US007070. 91US-00749446

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o;
                        CDNA sequence AAQ37477, encoding a neutrotrophic factor (NF), was derived from the native ciliary neurotrophic factor (CNTF) (e.g. EP-385060) by PCR amplification. In order to obtain a DNA sequence encoding the NF(1-180), a portion of the DNA sequence encoding AAB 76-180 of full-length CNTF was amplified using PCR from a bacterial expression vector, plasmid pSP18 and synthetic PCR primers AAQ37473 and AAQ37474. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                           63.0%; Score 12.6; DB 2; Length 34; 78.9%; Pred. No. 2e+04; ive 0; Mismatches 4; Indels
                                                                                                                                                                             Sequence 34 BP; 5 A; 9 C; 5 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 bp spacer DNA used in aptamer.
Example; Page 14; 34pp; English
                                                                                                                                                                                                                                                                                       2 GTAACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                       15 GIACCTICCAIGITIGIT 33
                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                   ABK91114 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aptamer; ss; sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIKE ) RIKEN KK.
(HAYA/) HAYASHIZAKI Y.
                                                                                                                                                                                                                                    Best Local Similarity
Matches 15; Conserv
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RESULT 41
AAQ37473
ID AAQ37.
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AC AAQ37.

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22-OCT-2001; 2001WO-US047856.
        WPI; 2002-608230/65
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                                                                                                                                                          WO200257414-A2.
  Hayashizaki Y;
                                                                                                                                                                                        Wohlgemuth J,
                                                                                                                                                     Homo sapiens.
                                                                                                                                                               25-JUL-2002.
                                                                                                                      ABZ00880;
                                                                                  Query Match
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                                                                                     Best Loca
Matches
                                                                                                           RESULT 43
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This invention relates to novel isolated aptamers comprising at least one base capable of base pairing and different from the standard Watson-Crick (W-C) bases. The invention also comprises a method for sequencing nucleic acids. The aptomers of the invention are useful for isolating a specific cids. The aptomers of the invention are useful for isolating a specific aptamer, mixing it with a pool of ligands, and recovering the specific aptamer. The aptomers of the invention are useful for detection of specific ligand from a biological sample, by selecting at least one specific aptamer, capable of binding to a specific selecting at least one specific aptamer with a biological sample, mixing the at least one specific one aptamer, and detecting the presence and/or quantity of the specific ligand from the biological sample bound to at least one aptamer. The aptamer of the invention is useful as a drug and for therspeutic treatment. The present sequence represents a 50 bp spacer oligonucleotide used in the construction of an aptamer of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
New aptamer comprising one base capable of base pairing and different from the standard Watson-Crick base, useful for isolating a specific ligand from a pool of ligands.
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Pred. No. 2.1e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50 BP; 15 A; 14 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                         Example 4; Page 23; 56pp; English.
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78.9%;
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Gaps
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                1 AGTAACATCTATGTTTGGT 19
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21 AGTGTCATCTATGTCGGGT 3 ABZ00880 standard; DNA; 50 BP 09-JAN-2003 (first entry)

177; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; Human leukocyte gene expression profiling probe SEQ ID NO 871.

20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.

(BIOC-) BIOCARDIA INC.

Prentice J, Phillips J; nuth J, Fry K, Matcuk G, Altman P, P:
Woodward R, Quertermous T, Johnson F;

New system for leukocyte expression profiling, diagnosing a disease, or

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligomucleotides (ABZ00010-ABZ00315) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

Claim 1; Page 432; Opp; English.

Phillips J;

Prentice J,

Johnson F; Altman P,

Quertermous T, Matcuk G,

Fry K,

WPI; 2002-636525/68. Wohlgemuth J, Fry Ly N, Woodward R,

(BIOC-) BIOCARDIA INC.

22-OCT-2001; 2001WO-US047856. 20-OCT-2000; 2000US-0241994P.

WO200257414-A2.

25-JUL-2002.

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                                                                          The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte gene expression profiling probe SEQ ID NO 3285.
                                                                                                                                                                                                                                                                                                                     Score 12.6; DB 6; Length 50;
Pred. No. 2.1e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                     Sequence 50 BP; 12 A; 10 C; 11 G; 17 T; 0 U; 0 Other;
                                                Claim 1; Page 352; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                      1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                     28 AGAAACACCCTTGTTTGGT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ03294 standard; DNA; 50 BP.
                                                                                                                                                                                                                                                                                                                   63.0%;
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Best Local Similarity 78.9°
Matches 15; Conservative
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for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting thesese complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, rishes allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructing strains for identifying gene products as effective targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida gene related tetracyclin promoter PCR primer SEQ ID NO 3069
                                                                                                                                                                                                                                                                                                               Score 12.6; DB 6; Length 50; Pred. No. 2.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                               Sequence 50 BP; 13 A; 11 C; 11 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 AGTAACATGAATGTTGT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ28986 standard; DNA; 55 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2001; 2001WO-US049486.
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                  63.0%;
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                                                                                                                                                                                                                                                                                                                                                Local Similarity 78.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-566694/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200253728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ28986;
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Matches
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AB228986

ID AB228986

ID AB228986

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ID AB2
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying con allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion, of a promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells in which both alleles modified are useful for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon

Claim 76; SEQ ID NO 3069; 167pp + Sequence Listing; English

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                translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a PCR primer used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
transporter, transcriptional,
                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                               63.0%; Score 12.6; DB 6; Length 55; 78.9%; Pred. No. 2.1e+04;
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Best Local Similarity
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848, App 848, App 145, App 145, App 3025, App 3034, Ap 10981, Ap 1523, Ap 1523, Ap 3034, Ap

Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

548, App 216, App 3, Appli 58587, A 58595, A

Sequence Seq

us-10-798-923a-36.szlm80.rnpb

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Sequence:

Searched:

Database

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US-09-877-478-848

US-03-42-902-145

US-10-342-902-145

US-10-669-841-145

US-10-669-841-145

US-10-669-841-145

US-10-669-841-145

US-10-688-706-3025

US-10-688-706-3025

US-10-688-706-3025

US-10-215-112-6231

US-10-215-112-6231

US-10-098-2638-15313

US-10-098-2638-1712

US-10-098-2638-29113

US-10-098-2638-29113

US-10-098-2638-29113

US-10-098-2638-29113

US-10-098-2638-1861

US-10-098-2638-1861

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US-10-098-2638-1861

US-10-098-2638-1981

US-10-113-187-871

US-10-098-2638-1981

US-10-113-187-871

US-10-098-2638-1981

US-10-113-187-871

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Sequence 2763, Ap
Sequence 37, Appli
Sequence 27, Appli
Sequence 17106, A
Sequence 1817, Ap
Sequence 2863, Ap
Sequence 2863, Ap
Sequence 14, Appl
Sequence 145, Appl
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Sequence 60525, A
Sequence 46, Appl
                                                                                                                                    September 23, 2004, 15:56:54 ; Search time 220 Seconds (without alignments) 460.450 Million cell updates/sec
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(cgn2_6/ptodata/2/pubpna/USG7_PUBCOMB.seq:*
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(cgn2_6/ptodata/2/pubpna/USG6_NEW_PUB.seq:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S US-10-9842-776A-46

S US-10-428-339-5

T US-10-688-706-2763

S US-10-043-639A-3

S US-10-043-639A-3

S US-10-099-263B-17106

US-09-911-132A-27

US-09-969-373-3917

US-10-688-706-2863
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US-10-032-585-3574
US-09-877-478-145
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                                                                                                                                                                                                                                                                                                                                                                    3337386 seqs, 2532474682 residues
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Listing first 150 summaries
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Perfect score:
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Sequence 58587, A
Sequence 58587, A
Sequence 1187, Ap
Sequence 2716, Ap
Sequence 2716, Ap
Sequence 2713, A
Sequence 2733, A
Sequence 35372, A
Sequence 35372, A
Sequence 128010,
Sequence 128010,
Sequence 272, App
Sequence 273, A
Sequence 274, App
Sequence 274, Ap
Sequence 27446,
Sequence 1882, A
Sequence 27446,
Sequence 175446,
Sequence 17546,
Sequence 1754

Sequence 26, Appl Sequence 21, Appl

Sequence Sequence Sequence Sequence

Sequence Sequence

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Indels

Query Match 76.0%; Score 15.2; DB 15; Best Local Similarity 85.0%; Pred. No. 2.2e+03; Matches 17; Conservative 0; Mismatches 3;

; TYPE: DNA ; ORGANISM: Rat US-10-059-273-6

1 AGTAACATCTATGTTTGGTT 20

25

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Length 37;

APPLICANT: Agoston, Denes V.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
FILE REFERENCE: 268422000100
CURRENT PAPLICATION NUMBER: US/10/059,273
CURRENT PILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/265,113
PRIOR PAPLICATION NUMBER: US 60/265,113
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEG I

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US-10-098-263B-60525

US-10-098-263B-60525

Sequence 60525, Application US/10098263B

Publication No. US2003104410A1

GENERAL INFORMATION: Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.118.105/1098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

FRIOR PILING DATE: 2001-03-6

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

1.ENGTON 10 60525
                                            Sequence 21, Appl
Sequence 21, Appl
Sequence 10835,
Sequence 2172, App
Sequence 2172, App
Sequence 2172, App
Sequence 2172, App
Sequence 1336, App
Sequence 1336, App
Sequence 1336, App
Sequence 1336, App
Sequence 226, Appl
Sequence 226, Appl
Sequence 2100, App
Sequence 210, Appl
Sequence 210, Appl
Sequence 210, Appl
Sequence 210, Appl
Sequence 226, Appl
Sequence 31622, Appl
Sequence 3162, Appl
Sequence 3132, Appl
Sequence 3132, Appl
Sequence 3132, Appl
Sequence 3133, Appl
Sequence 1982, Appl
Sequence 1982, Appl
Sequence 1982, Appl
Sequence 1982, Appl
Sequence 1983, Appl
Sequence 1984, A
US-10-124-747-21
US-10-604-21
US-10-607-204-21
US-10-607-204-21
US-10-607-204-21
US-10-608-263B-19514
US-10-098-263B-19514
US-10-098-263B-19514
US-10-098-263B-19306
US-10-075-169-2172
US-10-175-169-2172
US-10-171-173-185
US-10-171-173-185
US-10-171-170-520
US-10-170-170-520
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US-09-770-633-19
US-10-339-268A-37
US-10-339-268A-47
US-10-349-143-2712
US-10-066-543-3085
US-10-035-833A-3842
US-10-035-833A-3842
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US-09-908-975-6137
US-09-908-975-10839
US-09-908-975-11387
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                                                                138
c 139
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ALIGNMENTS

US-10-059-273-6/c; Sequence 6, Application US/10059273; Publication No. US20030170736A1; GENERAL INFORMATION:

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RESULT 3

US-09-642-776A-46

i Sequence 46, Application US/09842776A

i Sequence 46, Application No. US20040023316A1

i GENERAL INFORMATION:

i TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS

i TITLE OF INVENTION: IN THE STOOL

i FILE REFRENCE: 41732

i CURRENT APPLICATION NUMBER: US/09/842,776A

i CURRENT APPLICATION NUMBER: PCT/EP99/08212

i RIOR FILING DATE: 1999-10-29

i NUMBER OF SEQ ID NOS: 64

i SOFTWARE: Patentin Ver. 2.1

i SEQ ID NO 46

i SEQ ID NO 46

i SEQ ID NO 46

i LENGTH: 33
3 AGTAACATCGATGTTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Gaps

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Indels

72.0%; Score 14.4; DB 15; 93.8%; Pred. No. 4.8e+03; ive 0; Mismatches 1;

Query Match
Best Local Similarity 93.8
Matches 15; Conservative

; TYPE: DNA ; ORGANISM: Homo sapien US-10-098-263B-60525

LENGTH: 25

16

1 AGTAACATCTATGTTT

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                        Description of Artificial Sequence: DNA encoding
                ; OTHER INFORMATION: complementarity determining region (CDR1) of an ; OTHER INFORMATION: antibody light chain directed to a beta-urease ; OTHER INFORMATION: epitope (alternative sequence)
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. OTHER INFORMATION: Description of Artificial Sequence; note = CTHER INFORMATION: Synthetic construct
US-10-428-339-5
                                                                                                                                                                           Query Match 69.0%; Score 13.8; DB 13; Length 33; Best Local Similarity 88.2%; Pred. No. 9.4e+03; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%; Score 13.8; DB 16; Length 77; 88.2%; Pred. No. 1.1e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pharmacia Corp.
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REPERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: PATENTIN version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10428339
; Bublication No. US20030228612A1
; GENERAL INFORMATION:
APPLICANT: KENWARD, Kimberly D.
APPLICANT: SALEHUZZAMAN, Shah
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT EPIDERMAL;
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT EPIDERMAL;
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT EPIDERMAL;
CURRENT FILING DATE: 2003-04-30
; CURRENT FILING DATE: 2003-04-30
; PRIOR PELICATION NUMBER: 60/377,294
; ROOF FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FRRESEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 5
: LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2763, Application US/10688706; Publication No. US20040102412A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    4 AACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                 13 AACATTAATGTTTGGTT 29
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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US-10-688-706-2763/c
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LENGTH: 20
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FEATURE:
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APPLICANT: SARCARAL,
APPLICANT: SCOUZILLE, PATRICIA
APPLICANT: SCOUZILLE, PHILIPPE
TITLE OF INVENTION: METHOD FOR PREPARING 1,3-PROPANEDIOL BY A RECOMBINANT
TITLE OF INVENTION: MICRO-ORGANISM IN THE ABSENCE OF COENZYME B12 OR ONE OF
TITLE OF INVENTION: ITS PRECURSORS
TITLE OF INVENTION: ITS PRECURSORS
TITLE OF INVENTION: ITS PRECURSORS
TILLE OF INTURIOR OF TELLING DATE: 2003-04-12
CURRENT FILING DATE: 2003-04-12
PRIOR PLICATION NUMBER: PR 99/08939
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SSOTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 28
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Sequence 27, Application US/09911132A

Publication No. US20030096341A1

GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: Expression of Alkaline Phosphatase in Yeast
FILE REFERENCE: RDID 0073US
CURRENT APPLICATION NUMBER: US/09/911,132A
CURRENT FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 73
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  Length 20;
                                             Indels
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Score 13.6; DB 17;
Pred. No. 1.1e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.6; DB 15;
Pred. No. 1.1e+04;
0; Mismatches 4;
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Pred. No. 1.3e+04;
0; Mismatches 4;
                                                                                                                                                                                                                            Sequence 3, Application US/10043639A Publication No. US20030175916A1 GENERAL INFORMATION:
                                                                                     1 AGTAACATCTATGTTTGGTT 20
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                                                                                                                          20 ATTTATATCTAAGTTTGGTT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Clostridium butyricum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 80.0%;
Matches 16; Conservative (
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Best Local Similarity 80.0%;
Matches 16; Conservative
    Query Match
Best Local Similarity 80.0%;
Matches 16; Conservative
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; Sequence 2866, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
; APPLICANT: Broachat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REPERENCE: 01393/1
; CURRENT FILING DATE: 2003-10-17
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 3071
; SGPTWARE: PatentIn version 3.2
; SEQ ID NO 2868
; LENGTH: 20
                                                                                                                                                                                                                                                            Query Match 66.0%; Score 13.2; DB 17; Length 20; Best Local Similarity 83.3%; Pred. No. 1.7e+04; Matches 15; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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GRODEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE COMPUTER: 1BM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0%; Score 13.2; DB 17;
83.3%; Pred. No. 1.7e+04;
ive 0; Mismatches 3;
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CORRESPONDENCE ADDRESS:
ADDRESSE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                             ; OTHER INFORMATION: human GFAT antisense US-10-688-706-2863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: human GFAT antisense US-10-688-706-2868
PRIOR APPLICATION NUMBER: 60/419,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-753-143-14
Sequence 14, Application US/09753143
Patent No. US20020102550A1
GENERAL INFORMATION:
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                  PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 2863
LENGTH: 20
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10016
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                                                                                                                           TYPE: DNA ORGANISM: artificial
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US-10-688-706-2868/c
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                                                                                                                                                                        FEATURE:
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Matches
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                                 ; Sequence 17106, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
APPLICANT: Mitthan, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR PLLING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 17106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Squence 3917, Application US/09969373
Fatent No. US202013852A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
TITLE OF INVENTION: Soybean SSR8 and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR PILING DATE: 2001-01-05
PRIOR PILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25;
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APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.4; DB 15;
Pred. No. 1.4e+04;
0; Mismatches 1;
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Pred. No. 1.7e+04;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3,
Best 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-17106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Glycine max US-09-969-373-3917
                    US-10-098-263B-17106/c
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Gaps

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US-09-877-478-148

US-09-877-478-148

US-09-877-478-148

PUDICATION OF US20030068301A1

GENERAL INFORMATION:

PAPLICANT: Draper, Kenneth

APPLICANT: Draper, Kenneth

APPLICANT: Draper, Kenneth

APPLICANT: Moriseev, Jum

APPLICANT: Moriseev, Jum

APPLICANT: Moriseev, Jum

APPLICANT: Moriseev, Method and Reagent for Inhibiting Hepatitis B Virus Replication

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

CURRENT PILING DATE: 1992-60-14

PRIOR PLILING DATE: 1992-60-14

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR PELING DATE: 1994-02-07

PRIOR PELING DATE: 1994-02-07

PRIOR PELING DATE: 1995-06-04

PRIOR APPLICATION NUMBER: US 08/434,504

PRIOR APPLICATION NUMBER: US 08/434,430

PRIOR APPLICATION NUMBER: US 08/434,504

PRIOR APPLICATION NUMBER: US 08/434,504
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; Sequence 848, Application US/09877478
; Sequence 848, Application US/09877478
; Publication No. US2003068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Draper, Kenneth
; APPLICANT: McWiggen, Jim
APPLICANT: McWiggen, Jim
; APPLICANT: McWiggen, Jim
; APPLICANT: McWiggen, Jim
; TITLE OF INVENTION: McHood and Reagent for Inhibiting Hepatitis B Virus Replication
; TITLE OF INVENTION: McHood and Reagent for Inhibiting Hepatitis B Virus Replication NUMBER: US 09/09/877,478
; FRIOR APPLICATION NUMBER: US 09/696,31,025
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR PILING DATE: 2000-08-09
; PRIOR FILING DATE: 2000-08-09
; PRIOR FILING DATE: 1994-02-07
; PRIOR FILING DATE: 1994-02-07
; PRIOR FILING DATE: 1995-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGTAACATCTATGTTT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Hepatitis B virus US-09-877-478-145
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US-10-032-585-3574

US-10-032-585-3574

Sequence 3574, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:
APPLICANT: Terry, Koemer D.
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT APPLICATION NOWER: 2001-12-20
NUMBER OF SEQ ID NOS: 8000

SOFTWARE: PatentIn version 3.1
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Pred. No. 2e+04;
0; Mismatches 3;
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,143
APPLICATION NUMBER: US/09/753,143
FILING DATE: 02-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/175,828
FILING DATE: 1998-10-20
ATTORNEY/AGENT INFORMATION:
RAFFERENCE/DOCKET NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 39,911
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 687-595
TELEFAX: (212) 286-0854 OR 286-0082
TELEFAX: (212) 286-0854 OR 286-0082
TELEX: TWX 710-581-4766
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: «UNKNOWN»
DESCRIPTION: OTHER NUCLEIC ACID
MAND OTHERICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
OPERATING SYSTEM: MS-DOS
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Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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LENGTH: 65
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APPLICANT: MCSWiggen, Jim
APPLICANT: MCSWiggen, Jim
APPLICANT: MOSTISSEY, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REPERENCE: 400/075 (WHBB0-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR PILING DATE: 2000-06-08
PRIOR PILING DATE: 2000-06-08
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1992-06-14
PRIOR FILING DATE: 1993-06-14
PRIOR FILING DATE: 1993-06-14
PRIOR FILING DATE: 1994-02-07
PRIOR PRILING DATE: 1995-06-14
PRIOR PRILING DATE: 1995-06-14
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Demnis, Macejak
APPLICANT: Demnis, Macejak
APPLICANT: Demnis, Macejak
APPLICANT: Demnis, Macejak
APPLICANT: David, Morriseey
APPLICANT: David, Morriseey
APPLICANT: Pawela, Pavco
APPLICANT: Pawela, Pavco
APPLICANT: Partice, Lee
APPLICANT: Renneth, Drapet
APPLICANT: Renneth, Drapet
TITLE OF INVENTION OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED
TITLE OF INVENTION OLIGONUCLEOTIDE MEDIATE
TITLE OF INVENTION OLIGONUCLEOTIDE
TITLE OF INVENTION WURBER: US/10/669,841
CURRENT APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-11-2-5
PRIOR PELICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2002-02-10
PRIOR FILING DATE: 2002-03-16
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-16
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 60/30-06
PRIOR FILING DATE: 2000-12-18
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50.0%; Pred. No. 2.5e+04;
cive 6; Mismatches 2;
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Publication No. US20040127446A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGTAACATCTATGTTT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 50.0
Matches 8; Conservative
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TILE OF INVENTION: Mcthod and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MSHBOD-845-I)
CURRENT PILING DATE: 2003-01-15
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1992-05-14
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Pred. No. 2.5e+04;
6; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR PILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PATENTIN VETRION 3.0
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-342-902-145; Sequence 145, Application US/10342902; Publication No. US20040054156A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 848, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
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APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                 Similarity 50.0%; 8; Conservative (
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SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                       ; ORGANISM: Hepatitis B virus US-09-877-478-848
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ORGANISM: Hepatitis B virus
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                       Sequence 3025, Application US/10688706
; Sequence 3025, Application US/10688706
; Publication No. US2040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REPERENCE: 0.1393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SEQ ID NO 3025
; LENGTH: 20
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Publication No. US2004010241241
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR PPLICATION UNMBER: 60419,268
PRIOR FILING DATE: 2002-10-17
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Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2;
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US-10-688-706-3034
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US-10-215-112-6520
; Sequence 6520, Application US/10215112
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SOFTWARE: Patentin version 3.2
SEQ ID NO 3034
LENGTH: 20
                                                                            2 AGGAACCUCUAUGUUU 17
                                           1 AGTAACATCTATGTTT 16
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APPLICANT: David, Moritsesy
APPLICANT: Panela, Pavics
APPLICANT: Panela, Pavics
APPLICANT: Panela, Pavics
APPLICANT: Panela, Pavics
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION OLIGARICATION WINDS. (MHRDA-249-E)
TITLE OF INVENTION: VIROS REPLICATION
TITLE OF INVENTION WINDSER: PCT/USO2/09187
PRIOR PAPLICATION NUMBER: US 60/296, 87
PRIOR PAPLICATION NUMBER: US 60/335, 059
PRIOR PAPLICATION NUMBER: US 60/335, 124
PRIOR PILING DATE: 2001-02-2
PRIOR PAPLICATION NUMBER: US 60/335, 124
PRIOR PAPLICATION NUMBER: US 60/343, 124
PRIOR PAPLICATION NUMBER: US 60/343, 124
PRIOR PAPLICATION NUMBER: US 60/410, 332
PRIOR PAPLICATION NUMBER: US 60/410, 331
PRIOR PAPLICATION NUMBER: US 60/611, 931
PRIOR PAPLI
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PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: Patentin version 3.0
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64.0%; Score 12.8; DB 17; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.5e+04;
Matches 8; Conservative 6; Mismatches 2; Indels (
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Publication No. US20040127446A1
GENERAL INFORMATION:
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Sequence 3303, Application US/10775169
Fublication No. US20040175743A1
GRNERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Trepicchio, William
ITILE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
LENGTH: 25
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SOSTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 66526
LENGTH: 25
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                                                                                              Query Match 64.0%; Score 12.8; DB 15; Best Local Similarity 87.5%; Pred. No. 2.6e+04; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/099,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                Sequence 60526, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TILLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
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                                                                                                                                                                                                                                             1 AACGICTAICTITGGI 16
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) ORGANISM: Homo sapien
US-10-098-263B-60526
                       ; ORGANISM: Homo sapien
US-10-098-263B-1523
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US-10-098-263B-60526
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Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittenan, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT APPLICATION NUMBER: 60/276,759

PRIOR PELING DATE: 2001-01-08

NUMBER OF SEQ ID NOS: 131066

SOFTWARE MICROARRAY Probe Sequence Listing Generator V 1.1

LENGTH: 25
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; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFFWARR: FESTSEQ for Windows Version 4.0
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                 GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
TITLE OF INVENTION: Test3
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT APPLICATION NUMBER: 2002-08
NUMBER OF SEQ ID NOS: 14936
SEQ ID NOS: 14936
SEQ ID NO 6520
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-215-112-6520
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; CTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10981
                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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Publication No. US20030082596A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
US-10-098-263B-1523
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LENGTH: 25
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Indels

Length 25;

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TYPE: DNA ORGANISM: Artificial
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US-10-027-632-58587/c
                                                                                                                                                                                                                                                                       TYPE: DNA
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US-10-002-623-548
is equence 548, Application US/10002623
is publication No. US20030134285A1
is general information.
j APPLICANT: OBFNER, PETER A.
i TITLE OF INVENTION: A METHOD FOR DETERMINING GENETIC
i TITLE OF INVENTION: A PRILITATION, SUBSTRUCTURE AND GENE FLOW WITHIN HUMAN
i TITLE OF INVENTION: POPULATION
i FILE REFERENCE: STAN-212
i CURRENT PAPLICATION NUMBER: US/10/002,623
i CURRENT FILING DATE: 2001-11-01
i PRIOR APPLICATION NUMBER: US 60/245,355
i SOFTWARE: FastSEQ for Windows Version 4.0
i TANGTH: 23
i TANGTH: 23
i TANGTH: 23
i TANGTH: 2005-11-01
i NUMBER OF SEQ ID NOS: 952
i SOFTWARE: PastSEQ for Windows Version 4.0
i TANGTH: 23
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                                                                                                                               APPLICANT: Bulce, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
APPLICANT: TILLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031996-031000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 2278
SOFTWARE: Patentin version 3.2
SEQ ID NO 3304
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.0%; Score 12.8; DB 17; Length 25; Best Local Similarity 87.5%; Pred. No. 2.6e+04; Matches 14; Conservative 0; Mismatches 2; Indels
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US-10-168-445-216
; Sequence 216, Application US/10168445
; Publication No. US2030177518A1
; GENERAL INFORMATION:
; APPLICANT: OSDOURN, Anne E
; APPLICANT: Haralampidis, Kosmas
; APPLICANT: Bryan, Gregory T
; TITLE OF INVENTION: Plant Gene
; FILE REFERENCE: 0380-P02892USO
US-10-775-169-3304/c
; Sequence 3304, Application US/10775169
; Sequence 3306, US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                          Burczynski, Michael
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Best Local Similarity
Matches 14; Conserv
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; ORGANISM: probe
US-10-775-169-3304
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                                                                                                                        APPLICANT:
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Sequence 3, Application US/10353274

Sequence 3, Application US/20302358991

Fublication No. US203032358991

GENERAL INFORMATION:
APPLICANT: Agouron Pharmaceuticals, Inc.
TITLE OF INVENTION: CHALYTIC DOMAIN OF THE HUMAN EFFECTOR CELL CYCLE CHECKPOINT PROJECTIVE OF INVENTION: CHALYTIC DOMAIN OF THE HUMAN EFFECTOR OF INVENTION: KINASE, CHKI, MATERIALS AND METHODS FOR IDENTIFICATION OF INHIBIT FILE OF INVENTION UMBER: US10/353,274

CURRENT FILING DATE: 2003-01-28

PRIOR RILING DATE: 1999-12-14
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.128
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Segeunce: PCR primer US-10-353-274-3
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CURRENT APPLICATION NUMBER: US/10/168,445
CURRENT FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: PCT/GB00/04908
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-12-22
PRIOR FILING DATE: 1999-12-22
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 219
SOFTWARE: PatentIn version 3.0
SOFTWARE: 30
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SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 34
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GENERAL INCURRAILOW:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PELICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-04-20
FRIOR PELICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-03-24
FRIOR FILING DATE: 2000-03-24
FRIOR FILING DATE: 2000-03-24
FRIOR FILING DATE: 2000-03-24
FRIOR FILING DATE: 1999-11-23
FRIOR PELICATION NUMBER: US 60/156,358
FRIOR PELICATION NUMBER: US 60/156,358
FRIOR PELICATION NUMBER: US 60/146,002
FRIOR PELING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-08
FRIOR FILING DATE: 
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT FILMS DATE: 2002-04-30
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-329
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-08-38
FRIOR FILING DATE: 1999-08-38
FRIOR FILING DATE: 1999-08-09
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; Sequence 58595, Application US/10027632
; Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                              Publication No. US20030204075A9
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58587
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Fublication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
PRIOR PLILING DATE: 2000-07-12
PRIOR PLILING DATE: 2000-04-20
FRIOR PLILING DATE: 2000-04-20
FRIOR PLILING DATE: 2000-03-24
FRIOR PLILING DATE: 2000-03-24
FRIOR PLILING DATE: 1999-11-23
FRIOR PLILING DATE: 1999-11-23
FRIOR PLILING DATE: 1999-11-23
FRIOR PLILING DATE: 1999-108-09
FRIOR PLILING DATE: 1999-09-08
FRIOR PLILING DATE: 1999-09-08
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Pred. No. 2.8e+04;
1; Mismatches 3; Indels
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Pred. No. 2.8e+04;
L; Mismatches 3; Indels
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-08-28
PRIOR FILING DATE: 1999-08-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 58587
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58595
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US-10-027-632-58587/c
; Sequence 58587, Application US/10027632
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77.8%;
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 77.8'
Matches 14; Conservative
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US-10-027-632-58587
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US-10-027-632-58595
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Publication No. US20040102412A1

GENERAL INPORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: PRASTION: ANTISENSE MODULATION OF GFAT EXPRESSION

TITLE OF INVENTION: ANTISENSE: US/10/688,706

CURRENT APPLICATION NUMBER: US/10/688,706

CURRENT FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/419,268

PRIOR FILING DATE: 2002-10-17

SOFTWARE: PAPENTIN VERSION 3.2

SOFTWARE: Patentin version 3.2

LENGTH: 20
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Sequence 25123, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Score 12.6; DB 17; 78.9%; Pred. No. 3.1e+04; cive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.0%; Score 12.6; DB 15; 78.9%; Pred. No. 3.2e+04; ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: human GFAT antisense US-10-688-706-2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 27074, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGTAACATCTATGTTTGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GTAACATCTATGTTTGGTT 20
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    5 ACATCTATGTTTGGTT 20
                            43 ACALTTAIGTIIGIII 28
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Best Local Similarity 78.9°
Matches 15; Conservative
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Best Local Similarity 78.9
Matches 15; Conservative
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CORGANISM: Homo sapien
US-10-098-263B-25123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
US-10-098-263B-27074
                                                                                                                                   US-10-688-706-2716/c
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LENGTH: 25
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Fublication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION:

FILE REFERENCE: GENSET. 02020P1

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: EARLIER FILING DATE: 1999-10-20

PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-20

PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-20

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

FRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NOS: 11796
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APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Gharles, Bosney
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1712
LENGTH: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.8; DB 15; Length 43; Pred. No. 2.9e+04; 0; Mismatches 2; Indels
  Pred. No. 2.8e+04;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . LOCATION: 24
. OTHER INFORMATION: 99-7129-335 : polymorphic base A or C
JS-10-349-143-1887
                                                                                                                                                                                                                           ; Sequence 1712, Application US/10032585; Publication No. US20030180953A1; GENERAL INFORMATION:
                                                                     2 GTAACATCTAIGTTIGGT 19
                                                                                          64.0%;
87.5%;
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Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Candida albicans
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Best Local Similarity 87.5
Matches 14; Conservative
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ORGANISM: Homo Sapiens
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US-10-349-143-1887/c
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                                                                                     US-10-098-263B-36372/c

i Sequence 36372, Application US/10098263B

i Publication No. US20030104410A1

i GENERAL INFORMATION:
   APPLICANT: Mittman, Michael

i TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118-118-128-10-08

CURRENT PILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 06/276,759

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR APPLICATION NUMBER: 60/276,759

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 25;
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    Indels
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78.9%; Pred. No. 3.2e+04;
iive 0; Mismatches 4;
        4;
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      0; Mismatches
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3119.1
                                   2 GTAACATCTATGTTTGGTT 20
                                                               1 Gradcaggradgrircgri 19
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      15; Conservative
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Best Local Similarity 78.9
Matches 15; Conservative
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; ORGANISM: Homo sapien
US-10-098-263B-36372
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapien
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Matches 15; Conserv
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Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittenan, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 263B
CURRENT FILING DATE: 2003-01-08
FRIOR PEPLICATION NUMBER: 60/276, 759
FRIOR PILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Pred. No. 3.2e+04;
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                                                                                                                                                                                                          Length 25;
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 27074
LENGTH: 25
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Pred. No. 3.2e+04;
0; Mismatches 4;
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78.9%;
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Best Local Similarity 78.99
Matches 15; Conservative
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Matches 15; Conservative
                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-35597
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               RESULT 40
US-10-098-263B-29910/c
                                                                                                                                                                          US-10-098-263B-27074
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US-10-098-263B-100102
; Sequence 100102, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TILE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT APPLICATION NUMBER: 60/276,759
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 100102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.0%; Score 12.6; DB 15; Length 25; Best Local Similarity 78.9%; Pred. No. 3.2e+04; Matches 15; Conservative 0; Mismatches 4; Indels 0
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CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 65195
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GTAACAGGTAGGTTTCGTT 20
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CORGANISM: Homo sapien
US-10-098-263B-100102
                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-65195
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Sequence 14, Appl
Sequence 3, Appli
Sequence 1887, Ap
Sequence 5, Appli
Sequence 5, Appli
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149, Appl
3, Appl
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Sequence 11,
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(c) 1993 - 2004 Compugen Ltd.
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US-08-644-13-61
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Maximum Match 100%
Listing first 150 summaries
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99-479-0055 98-261-8220 10:0595-0774 90-208-7-796 90-208-746 88-320-373- 88-356-1711 88-956-1711 88-956-1711 98-956-1711 98-956-1711 98-956-1711 98-956-1711 98-956-1711 98-956-941.	88-398-617, 88-398-615, 88-397-303, 88-397-303, 88-435-501, 88-435-501, 88-435-601, 99-786-569, 88-398-615,	US-08-397-303-4 US-08-397-303-4 US-08-398-617-16 US-08-398-617-19 US-08-398-617-19 US-08-398-617-20 US-08-398-617-21 US-08-398-617-21 US-08-398-615-16 US-08-398-615-16 US-08-398-615-19 US-08-398-615-20 US-08-398-615-21 US-08-398-615-21 US-08-398-615-21 US-08-398-615-21 US-08-397-303-16 US-08-397-303-16	8-397-303-2 8-397-303-2 8-397-303-2 8-398-617-1 8-398-615-1 8-398-615-1 8-397-303-1 8-397-303-1 8-397-303-1 8-397-303-1 8-397-341-2 9-898-361-8 8-654-623-05-2	9.599-488BB 8-676-818-8 8-670-222-1 8-500-222-1 7-779-704B- 8-612-895A- 8-185-949B- 9-093-29-82-246-2 9-482-246-2 1284-10562A
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RESULT 2
US-09-187-050-9
US-09-187-050-9
Sequence 9, Application US/09187050B
Patent No. 6043072
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate
TITLE OF INVENTION: Synthase, And Methods of Use
FILE REFERENCE: WSUR12423
CURRENT APPLICATION UNDER: US/09/187,050B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_difference
LOCATION: (1)...(43)
OTHER INFORMATION: PCR primer for synthesizing Tr295 truncation
OTHER INFORMATION: product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 43;
                                              Score 13.8; DB 3; Length 2 Pred. No. 5.3e+02; 0; Mismatches 2; Indels
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88.2%; Pred. No. 5.6e+02;
iive 0; Mismatches 2;
, OTHER INFORMATION: Antisense Oligonucleotide US-09-359-757-34
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Sequence 19, Appl
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Sequence 1110, Appl
Sequence 1111, Appl
Sequence 1111, Appl
Sequence 1113, Appl
Sequence 1113, Appl
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Sequence 804, App
Sequence 1200, Ap
Sequence 2933, Ap
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Sequence 20, Appl
Sequence 110, App
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Sequence 416, App
Sequence 33, Appl
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US-09-359-757-34

Sequence 34, Application US/09359757

Patent No. 6086346

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: William Gaarde

APPLICANT: Lex M. Cowsert

TILE OF INVENITION: ANTISENSE MODULATION OF MEKKS EXPRESSION

FILE REPERENCE: RTS-0078

CURRENT APPLICATION NUMBER: US/09/359,757

CURRENT PILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 34

LENGTH: 20
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US-08-54-57A-6
US-08-422-978-862
US-08-432-978-862
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US-08-434-099A-18
US-08-434-099A-18
US-08-434-099A-19
5252476-15
US-08-634-34
US-09-428-082B-1111
US-09-428-082B-1111
US-09-428-082B-1111
US-09-428-082B-11113
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Sequence 14, Application US/08559303B
| Patent No. 5824501
| GENERAL INFORMATION:
| APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA APPLICANT: GRODEN:
| TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF BLOOM'S SYNDROME NUMBER OF SEQUENCES: 78
| CORRESPONDENCE ADDRESS: ANSTER; ROTHSTEIN & EBENSTEIN STREET: 90 PARK AVENUE CITY: NEW YORK STATE: NEW YORK STATE: NEW YORK STATE: NEW YORK COUNTRY: U.S.A. COMPTRY: N.S.A. COMPTRY: D.S.A. COMPTRY: STATE: NEW YORK S
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APPLICATION NUMBER: US/08/559,303B
FILING DATE: NOVEMBER 15, 1995
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

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64.0%; Score 12.8; DB 4;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2;
          STEANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: OTHER NUCLEIC ACID
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
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Patent No. 6670167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AGTACCATCAATGATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AGTACCATCTATCTT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lundgren, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen, Ping
Anderson, Mark
Deng, Ya-Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kan, Chen Chen
Luo, Chun
                                                                                                                                                                                                                                                                                                         LOCATION:
1 IDENTIFICATION METHOD:
1 OTHER INFORMATION:
US-09-175-828-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaur, Smita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-460-421-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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| Patent No. 6221643
| GENERAL INFORMATION |
| APPLICANT: MATHAN A. ELLIS, JAMES GERMAN, AND JOANNA APPLICANT: GRODEN |
| TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT |
| TITLE OF INVENTION: OF BLOOM'S SYNDROME |
| NUMBER OF SEQUENCES: 78 |
| CORRESPONDENCE ADDRESS: ADDRESSE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                        | NAME: ELIZABETH A. BOGOSIAN | REGISTRATION NUMBER: 39,911 | REFERENCE/DOCKET NUMBER: 39,911 | REFERENCE/DOCKET NUMBER: 63475/65 | TELECOMUNICATION INFORMATION: TELEPHONE: (212) 697-5995 | TELERAX: (212) 286-0854 or 286-0082 | TELEX: TWX 710-581-4766 | INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303
FILING DATE: NOVEMBER: 1, 1995
ATTORNEY AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REPERENCE/DOCKET NUMBER: 3475/65
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEPAX: (212) 286-0854 or 286-0082
TELEPAX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/175,828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER NUCLEIC ACID
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 83.3
Matches 15; Conservative
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COTHER INFORMATION:

US-08-559-303B-14
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                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
TOPOLOGY: LINEAR
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DESCRIPTION:
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LOCATION:
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US-09-175-828-14
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APPLICANT: Margoslak, Steve
APPLICANT: Nguyen, Binh
APPLICANT: Nguyen, Binh
APPLICANT: Register, James
APPLICANT: Register, James
APPLICANT: Rassell, Anna Tempczyk
APPLICANT: Sarup, Jay
TITLE OF INVENTION: Catalytic Domain of the Human Effector Cell cycle
TITLE OF INVENTION: Methods for Identification of Inhibitors Thereof
FILE REPERENCE: 0125-0032
CURRENT APPLICATION NUMBER: US/09/460,421
CURRENT FILING DATE: 1999-12-14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 34
                                                            Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-09-460-421-3
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Query Match 66.0%; Score 13.2; DB 3; Length 24; Best Local Similarity 83.3%; Pred. No. 1e+03; Matches 15; Conservative 0; Mismatches 3; Indels
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RESULT 9
US-09-757-014-5/c
; Sequence 5, Application US/09757014
; Sequence 5, Application US/09757014
; Patent No. 6348342
; GENERAL INFORMATION:
; APPLICANT: O'Dwyer, Karen
Perry, Caroline
Perry, Caroline
; TITLE OF INVENTION: No. 6348342el Compounds
; VUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Score 12.6; DB 3; Length 24; 78.9%; Pred. No. 2e+03; ive 0; Mismatches 4; Indels
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ZIP: 19103-2793
COMPUTER READMELE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
                      STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre CITY: Philadelphia
                                                                        STATE: PA

COUNTRY: USA

ZIP: 19103-273

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FSAELSE for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,699A
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CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/868,699
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           PAPLICATION NUMBER: US/08/868,699A
FILING DATE: 04-JUN-1997
CLASIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10012
TELECOMMUNICATION INFORMATION:
TELECHOME: 215-994-2488
  ADDRESSEE: Dechert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GTAACATCTATGTTTGGTT 20
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SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
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Best Local Similarity 78.9
Matches 15; Conservative
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APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET. 020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-10-21
EARLIER FILING DATE: 1998-10-21
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-14-21
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APPLICANT: Roberts, Christopher J.
APPLICANT: Roberts, Christopher J.
TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-048
CURRENT APPLICATION NUMBER: US/09/315,793
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.0%; Score 12.8; DB 4; Length 47; Best Local Similarity 87.5%; Pred. No. 1.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
COCATION: 24
COTHER INFORMATION: 99-7129-335 : polymorphic base A or C
US-09-422-978-1887
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Patent No. 6204019
GENERAL INFORMATION:
APPLICANT: O'DWyer, Karen
APPLICANT: Perry, Caroline
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: No. 6204019el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-315-793-53/c
; Sequence 53, Application US/09315793
; Patent No. 6221597
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ORGANISM: Homo Sapiens
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NAME: Falk, Stephen T

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linear
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0
                                                                                                                                                                                                                                                                                                  63.0%; Score 12.6; DB 4; Length 24; 78.9%; Pred. No. 2e+03; Live 0; Mismatches 4; Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-009-913-223/c
; Sequence 223, Application US/09009913
; Patent No. 6087486;
; GENERAL INFORMATION:
; APPLICANT: AxyS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10012
RELECOMMUNICATION INFORMATION:
TELLEPHONE: 215-994-2488
TELLEFAX: 215-994-222
TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ
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REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.9°
Matches 15, Conservative
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Best Local Similarity 78.9%
....hes 15; Conservative
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LENGTH: 27 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-327-3231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                            US-09-757-014-5
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Sequence 3, Application US/07749446

Patent No. 5593857

GENERAL INFORMATION:
APPLICANT: Hischer, Edmund G.
APPLICANT: Tischer, Edmund G.
APPLICANT: Thompson, Stewart A.
TITLE OF INVENTION: PRODUCTION OF HOMOGENEOUS CILIARY
TITLE OF INVENTION: NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: California Biotechnology Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: California
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CALLCATION NUMBER: US/07/749,446
FILING DATE: 19911008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ballance, David J
APPLICANT: Courtney, Michael G
APPLICANT: Finnis, Christopher J A
APPLICANT: Sleep, Darrell
TITLE OF INVENTION: Medicine
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centeon L.L.C.
STREET: 1020 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-08-584-760A-50
; Sequence 50, Application US/08584760A
; Patent No. 6290953
; GENERAL INFORMATION:
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REFERENCE/DOCKET NUMBER: 28,117
REFERENCE/DOCKET NUMBER: PC43:
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-962-5860
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TENGTH: 34 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GTAACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 GTACCTTCCATGTTTTGTT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: King of Prussia
STATE: Pennsylvania
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Sequence 11, Application US/09086726

Sequence 11, Application US/09086726

Patent No. 6346378

GENERAL INFORMATION:

APPLICANT: Stanley, Christopher John
APPLICANT: Oruw, Henrik
APPLICANT: Oruw, Henrik

TITLE OF INVENTION: Nucleic Acid Analogs With A Chelating Functionality
FILE REFERENCE: 108382-08046

CURRENT APPLICATION NUMBER: US/09/086,726

CURRENT FILING DATE: 1996-05-24

PRIOR FILING DATE: 1996-05-24

PRIOR FILING DATE: 1994-11.22

PRIOR FILING DATE: 1994-11.25

NUMBER OF SEQ ID NOS: 11

SOUTWARE: PatentIn version 3.1

LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: The sequence of an intramolecular stem structure of an US-09-086-726-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.0%; Score 12.6; DB 4; Length 37; Best Local Similarity 78.9%; Pred. No. 2.1e+03; Matches 15; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.0%; Score 12.6; DB 3; Length 36; 78.9%; Pred. No. 2.1e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature; LOGATION: 1..36; COTHER INFORMATION: /function= "oligonucleotide 49" US-08-584-760A-49
APPLICATION NUMBER: 08/211,860
FILING DATE: 15-APR-1994
APPLICATION NUMBER: 08 9121815.6
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Naomi Biswas
REGISTRATION NUMBER: 38,384
REFERENCE/DOCKET NUMBER: 92H853-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION = 610/878-4224
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                        92H853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 GTCACAACTATTTTAGTT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GIAACAICIAIGITIGGIT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 AATAACATCTTTGCTTGTT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.0
Best Local Similarity 78.9
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

| LOCATION: 1..35

| OTHER INFORMATION: /function= "oligonucleotide 50"

US-08-584-7604-50
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,760A
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,760A
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Sequence 49, Application US/08584760A

Sequence 49, Application US/08584760A

PRECENT NO. 629030A

APPLICANT: Ballance, David J

APPLICANT: Courtney, Michael G

APPLICANT: Finnis, Christopher J A

APPLICANT: Finnis, Christopher J A

APPLICANT: Sleep, Darrell

TITLE OF INVENTION: Medicine

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Centeon L.L.C.

STREET: 1020 First Avenue

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: USA
                                                                                                                                                                        FILING DATE:

CLASSIFICATION: 424

RIOR APPLICATION DATE:

APPLICATION NUMBER: 08/211,860

FILING DATE: 15-APR-1994

APPLICATION NUMBER: 68 9121815.6

FILING DATE: 14-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Naomi Biswas

REGISTRATION NUMBER: 38,384

REGISTRATION NUMBER: 38,384

REGISTRATION NUMBER: 32,8853-1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ 1D NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 Dage pairs

TENGTH: 35 Dage caid

STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                     92H853-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NAMNTI-SENSE: NO
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Gaps

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Gaps

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8; Mismatches
; OTHER INFORMATION: for Codon 508 - wildtype US-09-270-140A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 225
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEO ID NO: 60
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.0
Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-629-001A-60
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US-09-270-140A-52

i Sequence 52, Application US/09270140A

j Patent No. 6361941

i GENERAL INFORMATION:
i APPLICANT: Toda, Alison
i APPLICANT: Toda, Alison
i APPLICANT: Todaris, Murray
i TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
i TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
i CURRENT APPLICATION NUMBER: US/09/270,140A
i CURRENT FILING DATE: 1999-03-16
i PRIOR FILING DATE: 1998-03-27
i NUMBER OF SEQ ID NOS: 96
i SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                   ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 203 Textile Buildling, 119 No. 5587300th Fourth Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: wildtype RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·
                                                                                                GENERAL INFORMATION:
APPLICANT: Malter, James S.
TITLE OF INVENTION: Method to Increase Regulatory Molecule
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Multing, Raasch, Gebhardt & Schwappach, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.0%; Score 12.2; DB 1; Length 34; 82.4%; Pred. No. 3.2e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,130A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muleting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 119.00010101
TELECOMMULCATION INFORMATION:
TELEPHONE: 612-305-1220
             RESULT 15
US-08-233-130A-3/c
: Sequence 3, Application US/08233130A
: Patent No. 5587300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGTAACATCTATGTTTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AGTAATATGTATGTATG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 34 base pairs
                                                                                                                                                                                                                                                                                                                                               ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                          COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-233-130A-3
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LENGTH: 22
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Sequence 139, Application US/08642274D
Patent No. 6200749
GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 229000033
CURRENT APPLICATION NUMBER: 1996-05-03
NUMBER OF SEQ ID NOS: 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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     Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                  ATAXIA-TELANGIECTASIA GENE AND ITS GENOMIC ORGANIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 48334
ZIP: 48334
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/629,001A
Query Match 60.0%; Score 12; DB 4; I Best Local Similarity 35.0%; Pred. No. 3.9e+03; Matches 7; Conservative 8; Mismatches 5;
                                                                                                                                  AKESULT 17
US-08-629-001A-60
Sequence 60, Application US/08629001A
Patent No. 5858641
SENERAL INFORMATION:
TITLE OF INVENTION: APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA
TITLE OF INVENTION: GENOMIC ORGANIZATION
NUMBER OF SEQUENCES: 139
CORRESPONDENCES: 139
CORRESPONDENCES: 139
CORRESPONDENCES: ADDRESSEE: Kohn & Associates
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5858661thwestern Hwy.
CITY: Farmington Hills
COUNTRY: US
```

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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenkeov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
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US-09-443-199C-847/c

I Sequence 847, Application US/09443199C

FREAD INFORMATION:
GENERAL INFORMATION:
FRIENCEMAT:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
FILE REFERENCE: 15966-534A
CURRENT APPLICATION NUMBER: US/09/443,199C

CURRENT APPLICATION NUMBER: 60,109,024

FRICH FILING DATE: 1998-11-17

NUMBER OF SEQ ID NOS: 1272

SOFTWARE: CuraGen Patent Formatter Version 0.9

SEQ ID NO 847

LENGTH: 51
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| LOCATION: (266)...(0)
| CTHER INFORMATION: 1 of 2 allelic variants (848 is other entry)
| NAME/KEY: misc_feature
| LOCATION: (0)...(0)
| COTHER INFORMATION: Accession number cg43949585
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60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 75.0%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 47;
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COTHER INFORMATION: 99-15423-223 : polymorphic base G or US-09-422-978-2712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 12; DB 4; I
85.7%; Pred. No. 4.1e+03;
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                                      ; Sequence 2712, Application US/09422978
; Patent No. 6537751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
                     US-09-422-978-2712
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Patent No. 5646156
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INTIBITION OF EOSINOPHIL
TITLE OF INVENTION: ACTIVATION THROUGH A3 ADENOSINE RECEPTOR ANTAGONISM
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Merck & Co., Inc.
STREET: P.O.Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence:intronic CTHER INFORMATION: sequence US-08-642-274D-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 12; DB 1; Length 45; 75.0%; Pred. No. 4.1e+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                             Length 30,
                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PR PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 25-APR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                             Query Match 60.0%; Score 12; DB 3; Best Local Similarity 75.0%; Pred. No. 4e+03; Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19219
TELECOMMUNICATION INFORMATION:
TELEPRAK: (908) 594-370
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGTAACATCTATGTTTGGTT 20
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                                                                                                                                                                                                                                                                                                                        1 AGTAACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                   10 AGTAACATGTATTTGCTGTT 29
                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 139 LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        both
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-233-009-51
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FILING DATE: January 5, 1996
APPLICATION WUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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IS-09-440-523-61
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
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Facture No. 6027889

GENERAL INFORMATION:
APPLICANT: Baranty, Francis
APPLICANT: Baranty, Francis
TITLE OF INVENTION: OUPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
TITLE OF INVENTION: COUPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
FILE REPERENCE: 19603/441

CURRENT APPLICATION NUMBER: 60/018,532
CARRENT APPLICATION NUMBER: 60/018,532
EARLIER APPLICATION NUMBER: 60/018,532
MUMBER OF SEQ ID NOS: 76
SOFTWARE PARENTING DATE: 1996-05-29
NUMBER OF SEQ ID NOS: 76
SEQ ID NO 61

LENGTH: 57
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       US-09-443-199C-848/c

Sequence 848, Application US/09443199C

Patent No. 6670464

GENERAL INFORMATION:
PAPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Nactin
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
TITLE OF INVENTION: NUMBER: US/09/443,199C

CURRENT APPLICATION NUMBER: US/09/443,199C

CURRENT FILING DATE: 1999-11-16

PRIOR FILING DATE: 1998-11-17

NUMBER OF SEQ ID NOS: 1272

SEQ ID NO 848

LINGTH: 51

LENGTH: 51
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LOCATION: (26) ... (0)
OTHER INFORMATION: 2 of 2 allelic variants (847 is other entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.0%; Score 12; DB 4; Length 51; Best Local Similarity 75.0%; Pred. No. 4.2e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%; Score 12; DB 3; Length 57; 100.0%; Pred. No. 4.2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (0)...(0)
CTHER INFORMATION: Accession number cg43949585
US-09-443-199C-848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 ATTACCATCTGTATTTAGTT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
US-08-864-473-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-864-473-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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APPLICANT: Charles Kunsch

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                         APPLICANT: Barany, Francis
APPLICANT: Lubin, Matthew
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING
TITLE OF INVENTION: COUPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
FILE REFERENCE: 19603/441
CURRENT APPLICATION NUMBER: US/09/440,523
CURRENT PILING DATE: 1999-11-15
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 61
LENGTH: 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: Primer JOTHER INFORMATION: Sequence US-09-440-523-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: AGCII TEXT

CURRENT APPLICATION DATA:

FILING DATE: 20-Oct-1997

CLASSIPICATION: UNMOREN: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIPICATION: AUNKNOWN>

PRIOR APPLICATION: AUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%; Score 12; DB 3; Length 57; 100.0%; Pred. No. 4.2e+03;
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; Sequence 4982, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
Sequence 61, Application US/09440523
Patent No. 6268148
GENERAL INFORMATION:
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42 AGAAAAGCTATGTATGCTT 61
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APPLICANT: Pacletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: IMMUNODERICIENCY VIRUS RECOMBINANT
TITLE OF INVENTION: IMMUNODERICIENCY VIRUS RECOMBINANT
TITLE OF INVENTION: DOXVIRUS VACCINE
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
ADDRESSER: Curtis, Morris & Safford
ADDRESSER: Cof William S. Frommer
STREET: 530 Fifth Avenue
STREET: S30 Fifth Avenue
STREET: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 12; DB 1; Length 63; Best Local Similarity 75.0%; Pred. No. 4.2e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                         Query Match 60.0%; Score 12; DB 4; Length 58; Best Local Similarity 75.0%; Pred. No. 4.2e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                           Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/303,275
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,382
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S:
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4982:
US-08-956-171E-4982
REPERENCE/DOCKET NUMBER: PE
TELECOMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4982:
SEQUENCE CHARACTERICTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 198, Application US/08303275 Patent No. 5766598
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGTAACATCTATGTTTGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 AGATAAATCTATGATTGGAT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
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Gaps
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Reguence 399, Application US/09479005A
Retent No. 6656731
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBH800-884-C
CURRENT FILING DATE: 2000-01-07
RIOR APPLICATION NUMBER: US 09/444,209
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-12-2
us-uw-303-275-1999/c

Sequence 199, Application US/08303275

Patent No. 576658

GENERAL INFORMATION:
APPLICANT: Pacletti, Enzo
APPLICANT: Tarteglia, James
APPLICANT: Cox, William I.

TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS RECOMBINANT
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS RECOMBINANT
TITLE OF INVENTION: POXVIRUS VACCINE
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cutis, Morris & Safford
ADDRESSEE: Cutis, Morris & Safford
ADDRESSEE: Cow William S. Frommer
CITY: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: USA
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/303,275
FILING DATE: 11-10W-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
PRICK PROMER: WILLIAM S.
PRICK PROMER: WILLIAM S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REGISTRANCE/DOCKET NUMBER: 454310-2420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGTAACATCTATGTTTGGTT 20
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INFORMATION POR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 75.0
Matches 15; Conservative
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Patent No. 565053
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 4.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.8; DB 1; Length 18;
Pred. No. 4.9e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3100
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    6; Mismatches
PRIOR APPLICATION NUMBER: US 60/059,473
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SCFTWARE: PatentIn version 3.0
SEQ ID NO 399
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 57, Application PC/TUS9507744A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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                                                                                                                                                                                                                                                   1 AGTAACATCTATGTT 15
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Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                         TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: YES
US-08-261-822A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                             US-09-479-005A-399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 30
PCT-US95-07744A-57
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FACELIA NO. 15.35248

FARELIANT: DEAIN, NICHOLAS M.
APPLICANT: MCKAY, Robert A.
APPLICANT: Deain, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Mero, Pam
APPLICANT: Mero, Pam
APPLICANT: Moro, ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0350
CURRENT APPLICATION NUMBER: US/09/287,796A
CURRENT FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: 09/130,616
EARLIER APPLICATION NUMBER: 09/130,629
EARLIER PILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 149
LENGTH: 20
TYPE: DNA
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APPLICANT: Trustees of The University of Pennsylvania
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
TITLE OF INVENTION: and Pathogens
WUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STRERT: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
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CUDNIKAT: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
FILING DATE: 15-JUNE-1995
CLASSIFPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y:
REGISTRATION NUMBER: 34,293
TRECOMMUNICATION INFORMATION:
met FOLLING NUMBER: 34,293
TRECOMMUNICATION INFORMATION:
met FOLLING NUMBER: 34,293
TRECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
59.0%; Score 11.8; DB 5;
Best Local Similarity 86.7%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 2;
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; Patent No. 6133246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (215) 568-3100
TELERAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 57,
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCTATATTTGGTT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULL NC
HYPOTHETICAL: NC
                                                                                                                                                                                                                                                                 USA
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US-09-287-796-149/c
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                                                                                                                                                                                                                                                                 COUNTRY:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jan van den Hurk and Peter Tijssen
APPLICANT: Jan van den Hurk and Peter Tijssen
TITLE OF INVENTION: Bovine Viral Diarrhea Virus Group II
TITLE OF INVENTION: gp53 Compositions and Methods
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.0%; Score 11.8; DB 1; Length 29; 86.7%; Pred. No. 5e+03; tive 0; Mismatches 2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,722
       FILING DATE: 10-NOV-1994
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 36 615
REPERENCE/DOCKET NUMBER: 1242-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0860
TELEPAX: (415) 324-0860
TELEPAX: (215) 324-0860
TELEPAX: (315) 324-0860
TENCHALION: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR AMPLICATION DATA:
APPLICATION NUMBER: 08/445,746
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/337,618
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/COCKET NUMBER: 1242-0001.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-008-722-10
; Sequence 10, Application US/09008722
; Patent No. 6015795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE: Primer 1A INDIVIDUAL ISOLATE: Primer 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GIAACAICIAIGITI 16
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.7
Matches 13; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCOMATION:

APPLICANT: MCKAY, Robert A.

APPLICANT: Monia, Brett

APPLICANT: Monia, Brett

APPLICANT: Wonia, Brett

APPLICANT: Wenia, Pam

APPLICANT: Mania, Brett

APPLICANT: Mania Brett

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS

TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

FILE REFERENCE: ISPH-0318

CURRENT APPLICATION NUMBER: US/09/130,616C

CURRENT APPLICATION NUMBER: 08/910,629

EARLIER FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 178

SEQ ID NO 149

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.7%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                    Query Match
Best Local Similarity 86.7%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,746
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
; OTHER INFORMATION: Synthetic sequence US-09-130-616-149
                                         FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-287-796-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 32
US-09-130-616-149/c
; Sequence 149, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ACATCTATGTTTGGT 19
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Gaps

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linear

TOPOLOGY:

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APPLICANT: Kuchler, Ernst
APPLICANT: Liebig, Hans-Dieter
APPLICANT: Liebig, Hans-Dieter
APPLICANT: Sern, Timothy
TITLE OF INVENTION: Expression of Mature Proteinase 2A, the
TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates
NUMBER OF SEQUENCES: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2014. Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
GAPLICANT: Charles Kunsch
GAPPLICANT: Charles Charles
GAPPLICANT: Charles Charles
GAPPLICANT: Charles Charles
GAPPLICANT: Charles
G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/320,373
FILING DATE: 11-0CT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,619
FILING DATE: 06-NOV-1992
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     Maurer-Fogy, Ingrid
Sommergruber, Wolfgang
Zophel, Andreas
Blaas, Dieter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              ; Sequence 2, Application US/08320373; Patent No. 5559025; Patent INFORMATION: APPLICANT: Ahorn, Horst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202) 466-0800
(202) 833-8716
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 86.7
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                           US-08-320-373-2/c
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APPLICANT:
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TELEX: 2
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APPLICANT: Skern, Timothy
TITLE OF INVENTION: Expression of Mature Proteinase 2A, the
TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates
TITLE OF INVENTION: Having an Inhibitory Effect
CORRESPONDENCE ADDRESS:
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Pred. No. 5e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                            2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,373
FILING DATE: 11-OCT-1994
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US 07/971,619
FILING DATE: 06-NOV-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
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LUNKESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Avenue, N.W.

STATE: D.C.

COUNTRY: USA
ZIP: 20036
MPUTTED TO THE TOWNS TOWNS
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Sommergruber, Wolfgang
Sophel, Andreas
Blaas, Dieter
Kuchler, Ernst
Liebig, Hans-Dieter
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
MATI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Primer 1A
US-09-008-722-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08320373
Patent No. 5559025
                                                                                                                                                                                                                                                                         59.0%;
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TELEFAX: (202) 833-8716
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               2 GTAACATCTATGTTT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGAAGATCTATGTTT 15
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                                                                                                                                                                                                                                                                                                                                                13; Conservative
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STRANDEDNESS: single
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Best Local Similarity
Matches 13; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
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US-08-320-373-1
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APPLICANT:
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US-08-320-373-1
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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-00c1-1997
CLASSIFICATION: <Unknown>
                                  FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INPORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/ACRET INDOMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5031:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PB248P1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4977, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GII H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELEPHONE: (240) 314-1224
                                                                                                                                                                                                                        TELEPHONE: (240) 314-1224
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INFORMATION FOR SEQ ID NO: 5031:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:
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Matches 13; Conservative
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STATE: Maryland
COUNTRY: USA
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US-08-956-171E-4977/c
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
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0
                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE DISKELE, 3.50 inch, 1.4Mb storage SOFWHARE: ASCII TEXT COMPUTER: MP CASTI TOWN DATE:

CURRENT APPLICATION DATE:

FILING DATE: 20-Oct-1997

CLASSIFICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY AGENT INPORMATION:

NAME: MARK J. Hyman

REGISTRATION NUMBER: 46,789

REFRENCE/DOCKET NUMBER: PB248PI

TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11.8; DB 4; Length 50;
Pred. No. 5.2e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCIT Text CURRENT APPLICATION DATA: APPLICATION NOMBER: US/08/956,171E FILIAG DATE: 20-OCC-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear sequence DESCRIPTION: SEQ ID NO: 2061: US-08-956-171E-2061
    STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5031, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
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INFORMATION FOR SEQ ID NO: 2061:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.73
Matches 13; Conservative
                                                   STATE: Maryland
                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-956-171E-5031
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Batent No. 6608183

GENERAL INPORMATION:
APPLICANT: Co. III, George N

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS

CURRENT APPLICATION NUMBER: US/09/462,941

PRIOR APPLICATION NUMBER: 60/652,516

PRIOR APPLICATION NUMBER: 60/652,516

PRIOR PILING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30

LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09462941
| Patent No. 6608183 | GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: Cox III, George N |
| TITLE OF INVERTION DELIVATIVES OF GROWTH Hormone and Related Proteins |
| TITLE OF INVERTION DELIVATIVES OF GROWTH HORMONE A152-1-PUS |
| CURRENT APPLICATION NUMBER: US/09/462,941 |
| CURRENT PLING DATE: 1997-07-14 |
| PRIOR PILING DATE: 1997-07-14 |
| NUMBER OF SEQ ID NOS: 41 |
| SEQ ID NO 29 |
| LENGTH: 66 |
| LENGTH: 66 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o;
                                                                                                                                        / Match 59.0%; Score 11.8; DB 4; Length 58; Local Similarity 86.7%; Pred. No. 5.2e+03; hes 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11.8; DB 4; Length 66;
Pred. No. 5.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.0%; Score 11.8; DB 4;
86.7%; Pred. No. 5.3e+03;
tive 0; Mismatches 2;
                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 4977: US-08-956-171E-4977
LENGTH: 58 base pairs
                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.0%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          2 GTAACATCTATGTTT 16
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Best Local Similarity 86.79
Watches 13; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                            RESULT 40
US-09-462-941-30
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                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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APPLICANT: Simmons, Laura C.
APPLICANT: Simmons, Laura C.
APPLICANT: Simmons, Daniel G.
TITLE OF INVENTION: Methods and Compositions for Secretion of Heterologous Proteir
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
CONNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Yansura, Daniel G.
TITLE YENGENIN Methods and Compositions for Secretion of Heterologous Protein NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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  Indels
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    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILLING DATE:
Mismatches
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                           Sequence 5, Application US/08398617
Patent No. 5747662
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REPERENCE/DOCKET NUMBER: P889
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1489
TELEFAX: 415/552-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08398617
Patent No. 5747662
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                           6 CATCTATGTTTGGTT 20
                                                                                  43 CATCTATGTTCGTTT 57
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 86.7 es 13; Conservative
13; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 43
US-08-398-617-6/c
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APPLICANT: Simmons, Laura C.
APPLICANT: Yangura, Daniel G.
TITLE OF INVENTION: Methods and Compositions for Secretion of Heterologous Protein
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                       0;
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86.7%; Pred. No. 5.3e+03;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: US/08/398,615 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08398615
Parent No. S840523
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: P889
TELECOMMUNICATION INFORMATION:
TELECPHONE: 415/25-1489
TELECPHONE: 415/25-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CATCTATGTTTGGTT 20
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415/225-1489
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 67 bases
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Best Local Similarity 86.7.
Sheet Local 3; Conservative
                                     TELEX: 910/371-7169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 bases
                                                                                                                                                                                                                                                                          13; Conservative
                 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                        Best Local Similarity
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US-08-398-615-6
                                                                                                                                                                    linear
TELEPHONE:
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                                                                                                                                                                    TOPOLOGY:
                   TELEFAX:
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Sequence 5, Application US/08398615

Sequence 5, Application US/08398615

Patent No. 5840523

Patent No. 5840523

PAPLICANT: Simmons, Laura C.

APPLICANT: Yansura, Daniel G.

TITLE OF INVENTION: Methods and Compositions for Secretion of Heterologous Protein NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 5.3e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERARIE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California ZTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FILLS, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: P889
TELECOMMUNICATION:
                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION STATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: P889
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERIZIUS:
LENGTH: 67 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.0%; Sco
Best Local Similarity 86.7%; Pro
Matches 13; Conservative 0;
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STRANDEDNESS: single
  California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-398-617-6
                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
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Search completed: September 23, 2004, 16:44:22 Job time : 59 secs

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C 5 13.6 68.0 80 28 BH902197 C 6 13.4 67.0 46 28 AZ581263 C 7 13.4 67.0 70 14 CD946310 C 8 13.4 67.0 75 9 AR936725 C 8 13.5 66.0 31 20 AR936725	10 13.2 66.0 31 2E	13.2 66.0 46 28 13.2 66.0 50 29 13.2 66.0 52 14 13.2 66.0 59 28	15 13.2 66.0 79 28 16 13 65.0 76 9 17 12 8 64.0 52 28 19 12.8 64.0 52 28	12.8 64.0 64 9 12.8 64.0 67 28 12.8 64.0 70 29	22 12.8 64.0 73 29 23 12.8 64.0 76 28	12.8 64.0 77 28 12.6 63.0 33 28	12.6 63.0 52 9 12.6 63.0 58 9	29 12.6 63.0 64 12 30 12.6 63.0 66 28	32 12.6 63.0 73 28 33 12.6 63.0 73 28 33 12 6 63.0 74 9	12.6 63.0 74 9 12.6 63.0 74 29	36 12.6 63.0 75 29 37 12.6 63.0 76 9	38 12.6 63.0 79 28	12.4 62.0 60 28	12.4 62.0 77 29	43 12.4 62.0 79 14 44 12.2 61.0 24 29	45 12.2 61.0 40 28 46 12.2 61.0 43 28	12.2 61.0 46 28	49 12.2 61.0 47 9 50 12.2 61 0 50 9	12.2 61.0 51 28 12.2 61.0 51 28	12.2 61.0 53 13 12.2 61.0 55 29	12.2 61.0 59 9 12.2 61.0 59 14	12.2 61.0 59 14 12.2 61.0 62 12	59 12.2 61.0 62 28 60 12.2 61.0 63 9	61 12.2 61.0 64 9 62 12.2 61.0 64 28	63 12.2 61.0 65 29 64 12.2 61.0 66 28	12.2 61.0 66 29 12.2 61.0 66 29	67 12.2 61.0 67 14	12.2 61.0 69 28 12.2 61.0 69 29 12.2 61.0 70 12	71 12.2 61.0 70 29	12.2 61.0 76 10	74 12.2 61.0 77 28 12.2 61.0 77 29 75 12.2 61.0 77 29 77 12 60.0 36 29	57 55 5:00 31
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: September 23, 2004, 15:30:50; Search time 1335 Seconds (without alignments) 447.373 Million cell updates/sec	Title: US-10-798-923A-36 Perfect score: 20 Sequence: 1 agtaacatctatgtttggtt 20	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 27513289 segs, 14931090276 residues	umber of	Minimum DB seq length: 0 Maximum DB seq length: 80	Post-processing: Minimum Match 0% Maximum Match 100%	Listing first 150 summaries	Database : EST:* 1: em_estba:*	2: em_esthum:* 3: em_estin:*	4: em_estmu:* 5: em_estov:*	6: em_estpl:* 7: em estro:*	8: em_htc:* 9: ob est:*	10. gb_est2:* 11. gb_est2:*	12: gb_est3:*	13: gb_est4:* 14: gb_est5:*	15: em_estfun:* 16: em_estom:*	17: em_gss_hum:* 18: em_gss_inv:*	em gss em gss	e e				29: gb_gss2:*		of the total score distribut		Result Query No. Score Match Length DB ID	14 2 71 0 42 00 CONCARD OF THE PROPERTY OF THE	2 13.6 68.0 51 29 BX547845 BX547845 Arabidops C 3 13.6 68.0 58 28 BZ287564 BZ287564 SALK 0209 C 4 13.6 68.0 73 28 BH811903 BH811903 SALK 0605	

BH902197 SALK 0914
AZ5181263 100369016
CD946310 REL 89 Ge
AV036725 AV036725
A2995788 ZM0281D15
BH9002806 SALK 1009
AZ646477 IM0512G02
AL937476 Arabidops
CB275049 Kuc2b01.y
BZ384046 SALK 1049
BH613705 SALK 0346
AL682075 AL682075
BH907881 SALK 0446
BH611539 SALK 0641
CA935569 SAUS 0641
CA935569 SAUS 0641
CA935569 SAUS 0635
CC020433 35911 19
BH611539 SALK 0641
CA935569 SAUS 0641
CA935569 SAUS 0635
CC020433 3591 119
BH611539 SALK 1319
BH64251 SALK 0641
CA935569 SAUS 0635
CC020433 3591 119
BH64251 SALK 0531
BH864251 SALK 0534
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BK533710 Arabidops
CC5266681 SALK 0556
AL74707 QW94004.x
BH855346 SALK 0859
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BH855346 SALK 0556
AL24700 CST99133
CC524790 CST99133
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CC524790 CST99133
CC524790 CST99133
CC524790 CST99133
CG544249 IM0256E07
CG660595
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BZ555012 GO005930
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BZ655012 GO005930

ALIGNMENTS	1 6/c BX203696 ION Danio rerio ON BX203696		Eukary Actino	CE 1 (bases 1 RS Humphray, S.	TITLE DIRECT SUDMISSION JOURNAL SUbmitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:	(7 end of BAC 223	•	FEATURES Location/Qualifiers source 142	/organism="Danio rerio" /mol_type="genomic DNA" /dh_vref="raxon"7955"	/clone="DKEY-223120" /tissue type="Testis"	/note="Vector pIndigoBAC-536" ORIGIN	y Match	U	2 GTAACATCTATGTTTGGTT	Db 29 GTAACAAGTATGTT 11		LOCUS BX447845 51 bp DNA linear GSS 02-JUL-2003 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-548H03-020587, genomic survey sequence.	N BX547845 BX547845	KEYWORDS GSS. SOURCE Arabidopsis thaliana (thale cress) OPCANTSM Arabidopsis thaliana	Eukaryota; Spermatophy	REFERENCE 1 AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.	and Weisshaar, B. A pipeline for automated high-	transformed lines uppublished uppublished	REFERENCE 2 AGTHORS ROSSO,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)	ased reverse	Li,Y., Strizho
AZ663202 1M0542P08 AA907731 oj93912.s AZ427738 1M0209123 CC325169 XL921 Bay	AJ235769 AJ235769 BM342828 fw48e01.y BM574161 fx59h05.y BQ077144 fz13b11.y BQ615017 fab21009.	BI705299 fr56f02.y BI840243 fs71d07.y BQ615523 fab27d09. BH866324 SALK 1011	BM025452 f878902.y BM025460 f878h02.y BM035463 f678h05.y	BM025535 f879h02.y BM342608 fw45h08.y	B1705096 Ir63e06.y BM025311 f576g11.y RM342786 fw48a02.v	BM529195 fy15b04.y BM530824 fy17c08.y	BM85811 fx25e05.y BM85811 fx24605.y AA721179 nz71q07.s	BI702768 fr60c11.y BI702934 fr66b03.y	BI702944 fr66d08.y BI702951 fr66f05.y BI705117 fr66i05.y	B1705263 fr55d12.y B1705319 fr55d5.y	BI708682 £857h11.Y BI709372 £863906.Y	BI839414 fs67g10.y BI840013 fs68c01.y	BI840171 fs70d04.y BI840206 fs70h01.y	BM025435 fs78e05.y BM025520 fs79e07.y		BM18319/ IW31101.Y BM186911 fv79e09.Y BM187146 fv82f08.v			BI702921 fr65e05.y BI703270 fe47c09.y hr703373 fa47c09.y		B1708690 ISSBA10.Y B1708802 ISSS@11.Y B1709177 fs60h03.v			B1840318 is72d09.y B1840399 is73d11.y BM025305 is76g04.y	BM025335 fB77b09.y BM025349 fB77d04.y BM025351 f877d06.y	BM025401 fs78a08.y
.0 37 28 .0 40 9 .0 43 28	60.0 47 9 AJ235769 60.0 49 12 BM42828 60.0 49 12 BM574161 60.0 49 13 BQ077144 60.0 50 9 AU102956	0. 50 12 0. 50 12 0. 50 12 0. 62 03	 	.0 51 12 .0 51 12 .0 51 12	.0 52 12	2000	.0 52 12	.0 53 12	0.0 53 12	53 12	53 12	0 53 12 0 53 12	.0 53 12	.0 53 12 .0 53 12 .0 53 12	1.0 53 12 1.0 53 12	0.0 53 12 0.0 53 12 0.0 53 12	53 12	53 12 0.0 53 12 0.0 53 12	0.0 54 12	0.0 54 12 0.0 54 12 0.0 54 12	0.0 0.0 54 12 0.0 54 12	54 12	0.0 54 12 0.0 54 12 0.0 54 12	0.0 54 12 0.0 54 12 0.0 54 12	0.0 54 12	0.0 54 12
12 6	862 833 844 112 865 112 87 112 87 112 87	88 89 12 90 12 69	1222	95 12 6 96 12 6	97 12 6	101 12 6	102 12 6 103 12 6 104 12 6	105 12 6	107 12 6	110 12 6	112 12 6	114 12 (116 12 6	119 12 6	121 12 (122 12 (123 12 (124 12 (12 (126 12 12 12 12 12 12 12 12 12 12 12 12 12	129 130 130	131 12	133 12 12 134 12 12 12 12 12 12 12 12 12 12 12 12 12	136 12 137 12 138	139	141 12 12 143 12 12	144 145 146 12	147 12 12 148 12	149 12 150 12

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Best Local Similarity
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BH811903/c
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                Submitted (01-JUL-2003) Weisshaar B., Max-Planck-Institut fuer Submitted (01-JUL-2003) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5909430. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mgg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="GK-548H03-020587"
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/clone="GK-548H03-020587"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HZ287564 GSS 24-OCT-2002 SALK 020942.48.40.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_020942.48.40.x, genomic survey sequence.
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 58)
Alonso, J.M., Leiske, T., Barajas, P., Chen, H., Cheuk, R.,
Shinn, P., Zimmerman, J. and Bcker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
IOU10 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3702"
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Class: TDNA tagged.
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BZ287564/c
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TITLE
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SOURCE
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.58
 /organism="Arabidopsis thaliana"

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BH811903 73 bp DNA linear GSS 02-MAY-2002 SALK 060502 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_060502, genomic survey sequence.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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/clone_lib="Arabidopsis_thaliana_TDNA_insertion_lines"
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
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GSS.
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Unpublished (2001)
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Best Local Similarity 80.v.
Past Local Similarity
Partine
Conservative
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Б

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Laboratory Mouse DNA Resources (duttp://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinae. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gilfalfalgalpAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 15-JUL-2003
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Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 70)
                                                                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="B. Coli strain XL:10-Gold, T1-resistant, F-"
/clone 11b="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42Iny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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REL 89 GeneTagl Zea mays cDNA, mRNA sequence.
CD946310
                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: N columm: 16
Seq primer: CACACAGGAACAGGTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Mus musculus"
                                                                                                                        plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 46.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="UUGC1M0369N16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GTTACATCTATGTTT 2
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1 (bases 1 to 80)

2 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Geske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Requence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

L Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torray Pines Road, La Jolla, CA 92037, USA

Tel: 858 558 6379
                                                                                                              SALK 091447 41.05.x Arabidopsis thaliana TDNA linear GSS 04-SEP-2002 Arabidopsis thaliana genomic clone SALK 091447.41.05.x, genomic BH902197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ581263 46 bp DNA linear GSS 13-DEC-2000 1M0369N16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0369N16 R, genomic survey sequence.
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: TDNA tagged.
Location/Qualifiers
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ACATGINTGTTTGGTT 48
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Fax: 801 585 7177
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Popermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 75)
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/dev_stage="second leaf stage"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare seedling leaves second leaf stage"
                    Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
                                                                                                                                                      This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
database:http://www.rib.okayama-u.ac.jp/barley/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                   67.0%; Score 13.4; DB 14; Length 70; 93.3%; Pred. No. 5.8e+04; ive 0; Mismatches 1; Indels (
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                                                                                              93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.4; DB 9; 1
Pred. No. 5.8e+04;
0; Mismatches 2;
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cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="basdla13"
                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
/clone_lib="GeneTag1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                                             /organism="Zea mays"
                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="mixture"
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l Similarity 87.5%;
14; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwap42 (gil-#132114 [gb] ART25072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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   GSS 27-APR-2001
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Dlasmid inserts
Dlasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Female"
/lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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AZ995788 31 bp DNA linear GSS 27-APR-200
2M0281D15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0281D15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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83.3%; Pred. No. 6.4e+04;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 10000 Std Error: (Plate: 0281 row: D column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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High quality sequence stop: 31.
Location/Qualifiers
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/clone="UUGC2M0281D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                            AZ995788.1 GI:13867015
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Best Local Similarity 83.3
Matches 15; Conservative
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP(2 [qi|4712114]gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USS.

Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 46;
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Pred. No. 6.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                 Std Error: 0.00
                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.0
Plate: 0512 row: G column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Clate: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/61"
                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.
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/clone="UUGC1M0512G02"
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Location/Qualifiers
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83.3%;
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                                                                                                                                    plasmid inserts
Unpublished (2000)
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Best Local Similarity
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VERSION
KEYWORDS
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                AUTHORS
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I (bases 1 to 39)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

L. Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
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                                                                                                                                                                       BH902806 39 bp DNA linear GSS 04-SEP-2002 SALK 100993.19.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_100993.19.05.x, genomic
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Mararyota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
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/clone="XALK 100993.19.05.x"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5gl2870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
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                     1 AGTGACATGTGTGTTTGG 18
                                                                                                                                                                                                                                                                                                             BH902806.1 GI:22713922
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15; Conservative
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                                                                                                                                                                                                                                                        survey sequence.
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Best Local Similarity
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Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarten
at Washington University, St. Louis. This is a Oligo(dT)-SLI PCR
based library. CDNA PCR products of size >400 nucleotides
containing SLI on the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into pCRII-TOPO(Invitrogen) following the
Topo TA cloning protocol. Parasitic adult females were collected
from immunologically naive animals and provided by Dr. Mark Viney
(Mark Viney@bristol.ac.uk) of University of Bristol, Bristol, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCRII-TOPO (Invitrogen); Site_1: BCORI; Site_2: BCORI, The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. This is a Oligo(dr)-SL1 PCR based library. CDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dr) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following. the Topo TA cloning protocol. Parasitic adult females were collected from immunologically naive animals and provided by Dr. Mark Viney (Mark.Viney@bristol.ac.uk) of University of Bristol, Bristol, UK."
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.

1 (bases 1 to 59)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Strongyloides ratti PA female naive SL1 TOPO
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SALK 134985.22.65.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_134985.22.65.x, genomic
   Unpublished (1999)
Contact: McCarter De
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
Washington Box Box 8501, St. Louis, MO 63108, 7444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 741: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity 83.3%; Pred. No. 6.9e+04;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Strongyloides ratti"
/mol_type="mRNA"
/db_xref="taxon:34506"
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/lab_host="DH10B"
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The vector to vector length is 53
Seg primer: SLI primer.
Location/Qualiflers
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Unpublished (2001)
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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/clone="GK-081A08-016179"
/clone="GK-081A08-016179"
/clone="GK-081A08-016179"
/clone="FCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAc161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A, thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
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Strongyloides ratti
Strongyloides ratti
Strongyloides ratti
Strongyloides ratti
Eukaryota; Menatoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloidides;
E 1 (bases 1 to 52)
S McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Knoaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ku62b01.y1 Strongyloides ratti PA female naive SL1 TOPO v2 Strongyloides ratti cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-00T-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F14013. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on the availability can be found at:
                                                                                                                                                                                                                                       Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                               Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
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                                                     and Weisshaar, B.
A pipeline for automated high-throughput generation of F. (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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/strain="Columbia 0"
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Matches 15; Conservative
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CB275049/c
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Gaps

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ABLK 034815 Arabidopsis thaliana TDNA linear GSS 04-JAN-2002 SALK 034815 Arabidopsis thaliana genomic clone SALK 034815, genomic survey sequence. BH613705
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Clone="SALK 134985.22.65.x"

Clone="lb="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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/note="PCR was performed on Arabidopsis thaliana lines
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                                                                                                                                                   This is single pass sequence recovered from the left border of TDNA.
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                       1..59
/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
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/clone="SALK_034815"
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDNA.
Class: TDNA tagged
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                                                                                                                                                                                                      Class: TDNA tagged
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Best Local Similarity
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BH613705/c
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E Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Kanopus tropicalis EST project 2001 (11_2003)

Lipublished (2003)

On Mar 18, 2002 this sequence version replaced gi:19538449.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library

Constructed by Aaron M. Zorn.

CONA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13

gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with

EcoRI at the S' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI, Site 2: NotI

Host: Escherichia coli XII-blue
                                                                                                                                                                                                                                                                                                                                                                                                                               AL682075 AGC-gastrula Silurana tropicalis cDNA clone TGas058j17 5',
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each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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/lab_host="Escherichia coli XL1-blue"
/clone lib="XGC-gastrula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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TROPICALIS_SEQUENCE ID: TGas058j17.plcSP6
Sequencing primer: $P6.
Location/Qualifiers
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100.0%; Pred. No. 8.9e+04;
ive 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:8364"
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VERSION KEYWORDS

RESULT 17

3H907881

LOCUS

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A1930700
64 bp mRNA linear EST 30-NOV-2001
8D38611.y1 Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1013-357 5' similar to SW:G3PC DIACA P34931 GLYCERALDEHYDE
3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC ;, mRNA sequence.
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="SALK 059062"
/clone="SALK 059062"
/clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g54840. Class: TDNA tagged.
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand This clone is
available through: ResGen, Invitrogen Corp. 2130 South Memorial
Parkway Huntsville, AL 35801 For further information call:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
      Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
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                                                                                      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIG:
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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87.5%; Pred. No. 1e+05;
iive 0; Mismatches 2;
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/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
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                            Arabidopsis Genome
Unpublished (2001)
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Matches 14; Conservative
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                                                BH907881 44 bp DNA linear GSS 04-SEP-2002 SALK_044616.22.70.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_044616.22.70.x, genomic
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids; eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
dadtinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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1 (basea I to 52)
Alonso, J.W., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
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SALK 059062 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_059062, genomic survey sequence,
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/clome=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tes: 888 453 4100 x1752
Fex: 888 558 638 4100 x1752
Email: ecker@salk.edu
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/strain="Columbia 0"
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Query Match

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/gex="Male" | Journal of Strain XL10-Gold, T1-resistant, F-" | Jab host="E. Coli strain XL10-Gold, T1-resistant, F-" | Jab host="E. Coli strain XL10-Gold, T1-resistant, F-" | Clone 11b="Mouse 10kb plasmid UUGCIM library" | Mouse INF Mouse INF Plasmid UUGCIM library" | Mouse INF Mouse INF Strain | Mouse INF Strain Strain | Mouse INF Strain Str
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

L. Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
hl@sanger.ac.uk and
constructed at the Institute for Genomic Research (TIGR),
Rockville, M. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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T. brucei sheared genomic DNA clone 26h12, forward sequence,
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Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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                         'organism="Mus musculus"
                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC2M0024C04"
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SS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahnoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                /done lib="Gm-cloid"
//clone lib="Gm-cloid"
//clone lib="Gm-cloid"
//clone lib="Gm-cloid"
//clone This Cobn library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene planescript II XR cDNA library construction Kit.

Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were clareformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
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                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1013-357"
/tisue_type="whole seedlings, 2-3 week old seedlings, 2reanhouse grown"
/lab_host="XL10-Gold"
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(800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1417 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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Insert Length: 10000 Std Error: 0.00
Plate: 0024 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 67.
Location/Qualifiers
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Fax: 801 585 7177
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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1M0225K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0225K08 F, genomic survey sequence.
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1 (basea; Drosophilidae; Drosophila.

(basea; Drosophila, Zheng, Z., Chen.H.W., Chen, X., Wang, H., Ruan, P., Moody, M. and Hou, S.X.
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="l(2)5H1233"
/clone="lib="P-element-insertion screen"
    Query Match 64.0%; Score 12.8; DB 29; Best Local Similarity 87.5%; Pred. No. 1.1e+05; Matches 14; Conservative 0; Mismatches 2;
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ilarity 87.5%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 2;
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Fax: 1-301-846-6145
                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
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Genetics 163 (1), 195-201 (2003)
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Class: unknown
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Location/Qualifiers
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Lab. of Immunobiology
NCI-FCRDC
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3 (bases 1 to 73)

Strizhov, N. Li, Y., Rosso, M. and Weisshaar, B.

Direct Submission

Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNR. It

indicates an insertion within the locus defined by clone F5B19. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the German

Plant Genomics program designated 'GABI'. Information on line
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/note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAciso. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weisshaar,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana T-DNA flanking sequence GK-389F02-018268. genomic survey sequence.
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                      64.0%; Score 12.8; DB 29; Length 70; 87.5%; Pred. No. 1.1e+05; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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/mol type="genomic DNA"
/strain="Columbia 0"
1. .70
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="26h12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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/clone="GK-389F02-018268"
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                                                                                                                                                                                                                                                                                   4 AACATCTATGTTTGGT 19
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                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                              Local Similarity
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JOURNAL REFERENCE

TITLE

SOURCE

FEATURES

ORIGIN

COMMENT

TITLE

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Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA935569 51 bp mRNA linear EST 30-DEC-2002 sau56b06.yl Gm-c1071 Glycine max CDNA clone SOYBEAN CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker, R., Kehm, P., Vodkin, L., Brpelding, J., Coryell, V.,
Shoemaker, R., Reim, P., Vodkin, L., Brpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Frednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="SALK 04174.25.60.x"
/clone="SALK 04174.25.60.x"
/clone="Delta Trabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                             This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                        Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Pars: 858 558 558 579 Email: ecker@ealk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 12.6; DB 28; 78.9%; Pred. No. 1.2e+05; ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/strain="Columbia 0"
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Location/Qualifiers
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CA935569.1 GI:27424049
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Best Local Similarity 78.9
Matches 15; Conservative
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AUTHORS
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CA935569
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KEYWORDS
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Crosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
1 (bases 1 to 33)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD4Zny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                   S. 2030 E., SLC,
        Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                          Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0225 row: K column: 08
Seq primer: CGTrGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 77.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
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clone="UUGC1M0225K08"
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BH792403
BH792403.1 GI:19889138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="Male"
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Best Local Similarity 87.59
Matches 14; Conservative
                                                                       plasmid inserts
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                                                                                                                                                                                                                                                                                                         Jab host="DH10B"
/clone lib="Gm-c1071"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; The
cDNA library was constructed from mRNA isolated from
immature pods (approximately 2cm long) of greenhouse grown
plants. The library was prepared using the Life
Technologies pSuperScript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a NotI restrictions site. SalI
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-salI restriction
site of the pSPORTI vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinios at
Urbana-Champaign. email: l-vodkin@uiuc.edu"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 52)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
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zml2c05.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:525416 5' similar to TR:G545018 G545018 BRG1=BRAHMA HOMOLOG
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WARNING: There is evidence that suggests that the 384-well parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags denome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                          /clone="SOYBEAN CLONE ID: Gm-c1071-4692"
/tissue_type="immature pods (~2cm long) of greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.0%; Score 12.6; DB 14; Length 51; 78.9%; Pred. No. 1.3e+05;
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                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:
                                                                                                                                                                    organism="Glycine max"
                                            Putative full length read
vector to vector length is 52
Seq primer: -40RP from Gibco.
Location/Qualifiers
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AA065015.1 GI:1558631
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plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
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/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs two to
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosida II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV518688 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana clone APD36a04F 3', mRNA sequence.
                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -28N13 rev2 from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Contact: Brika Asamizu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%; Score 12.6; DB 9; 78.9%; Pred. No. 1.3e+05; iive 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                            1. .52
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:3916845"
                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:525416"
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/clone="APD36a04F"
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/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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Matches 15; Conserv
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1 AGTAACATCTATGTTTGGT 19
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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SWOV3MCAM61F08SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM61F08 5',
                 /note="Vector: pBluescript11 SK-; Site_1: EcoRI; Site_2:
Xho!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular Parasitology
Smith College Department of Biological Sciences
Smith College Department of Biological Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135833826
Fax: 4135833826
Fax: 413583346
Example Sequence Center, Smith
Sequence Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135833826
Fax: 413583346
Sequence Center, Smith
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/lab.host="XL1.Blue MRF'"
/clone lib="Orchocerca volvulus molting L3 larva cDNA
(SL96MLW-OrmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 64)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                                                       Gaps
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o
                                                                                                                  Score 12.6; DB 9; Length 58; Pred. No. 1.3e+05; 0; Mismatches 4; Indels
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/organism="Onchocerca volvulus"
/mol type=maxna"
/strain="Kumba, Cameroons"
/db xref="texon:6282"
/clone="SWOv3MCAM61F08"
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six-week old"
                                                                                                                    63.0%;
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                                                                                                                                                                    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                    Query Match
Best Local Similarity
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Gaps

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ch 63.0%; Score 12.6; DB 12; Length 64; 1 Similarity 78.9%; Pred. No. 1.3e+05; 15; Conservative 0; Mismatches 4; Indels (

Query Match Best Local Similarity Matches 15; Conserv

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gil 47321141gbl AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiilo-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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                                                                                                                                                                                 GSS 13-DEC-2000
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nederlly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                 AZ630914 66 bp DNA linear GSS 13-DEC-200
1M0485A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G77BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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ilarity 78.9%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 0485 row: A column: 05
Seg primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGCIM0485A05"
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48 AGAAGCATCTGTGTTTGAT 30
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/wiganism="Zea mays" |
/mol_type="ganomic DNa" |
/mol_type="ganomic DNa" |
/db_xref="taxon:4577" |
/tissue_type="leaf" |
/dev_stage="adult" |
/lab_host="DH10B" |
/clone_lib="3591 - RescueMu (engineered from DB1ueScript backbone); Site_l: BamHi; Site_2: BglII; |
/RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total agenomic DNa. RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total agenomic DNa. Not elements insert preferentially into transcription units: For more information on RescueMu, go to the web site 'www.rdmb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Moloka in 2002. DNA was extracted from leaf strips, double digested using BamHi and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 7)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Soldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Galdman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1904585 130-MAR-2000 14 bp mRNA linear EST 30-MAR-2000 IL-BT062-191298-010_1 BT062 Homo sapiens CDNA, mRNA sequence.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT062-010_1.ht
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Class: transposon-tagged.
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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78.9%; Pred. No. 1.4e+05;
tive 0; Mismatches 4;
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| AGTAACTGTTCTGTTTGGT 54
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Homo sapiens
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AI904585
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                                                                                                                                                                     CD826259 73 bp mRNA linear EST 10-JUL-2003
BN25.063E12F020118 BN25 Brassica napus cDNA clone BN25063E12, mRNA
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                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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1 (bases 1 to 73)
Walbot, V.
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica napus"
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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN25063E12"
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/clone_lib="BN25"
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                                                43 AGTAGCTTCTGGGTTTGGT
  1 AGTAACATCTATGTTTGGT
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1 Similarity 78.9%;
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                                                                                                                                                                                                                                                                                                                                           Brassica napus
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DR17E12S/c
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BX896687
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 74)
Diases 1 to 74)
Diases 1 to 74)
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                 /sex="female"
/dev stage="Adult"
/dev stage="Adult"
/clone_lib="BT062"
/note="Organ: Dreast; Vector: puc18; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/seq/gethtml.pl?t1=IL&t2=IL-BT062-011.html

&t3=311298&t4=1)

Seq primer: puc 18 forward.

Location/Qualifiers
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/clone_lib="BT062"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2:
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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IL-BT062-311298-011 BT062 Homo Bapiens cDNA, mRNA sequence.
AI904593
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                     Length 74;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
                                                             1. .74
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                               stringency conditions."
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/db_xref="taxon:9606"
ml&t3=191298&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
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Homo sapiens
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DR17E12S
Danio rerio genomic clone DKEY-17E12, genomic survey sequence.
AL734254
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This sequence was generated from the SP6 end of BAC 17E12. 17E12 is part of the Danlokey BAC Library created by R. Plasterk and N.V.
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Arabidopsis thaliana T-DNA flanking sequence GK-759A06-023802,
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Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the DUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
I (bases 1 to 74)
Humphray, S. J., Huckle, E. and Hunt, S. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1. .74
/organism="Danio rerio"
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/tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                         stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GTAACATCTATGTTTGGTT 20
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Matches 15; Conserv
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                           /mol_type="maxna"
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/clone="taxon:9606"
/tissue type="tumor, 5 pooled (see description)"
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/clone lib="NGI CGAP Ov35"
/clone lib="NGI CGAP Ov35"
/clone lib="NGI CGAP Ov23. Cloned unidirectionally.
Site 2: Not1, This library represents the normalized
version of NCI CGAP Ov23. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 0.86 kb. Tumor
types include: mixed Mullerian tumor, papillary serous,
clear cell, spindle cell. All are primary tumors,
metastasis positive. Constructed by Life Technologies."
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ358128 SALK 131965.28.05.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_131965.28.05.n, genomic
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
1010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
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/wol_type="genomic DNA"
                                                                                                                                                                             Trace considered overall poor quality Insert Length: 254 Std Error: 0.00
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                                                                                                                                                                                                           Insert Length: 254 Std Error.
Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           Submitted (15-DEC-2003) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone 1317. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mgo.de/GABI-Kat/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI648529 76 bp mRNA linear EST 16-DEC-1999 tz55a02.x1 NCI CGAP Ov35 Homo sapiens cDNA clone INAGE:2292458 3' similar to gb:M60278 HEPARIN-BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HUMAN);contains MSR1.t3 TAR1 repetitive element ;, mRNA
                                                                                                                                        Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
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1 (bases 1 to 76)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Banal: cgapbs-rémnal.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
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Pred. No. 1.4e+05;
0; Mismatches 4; Indels (
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Rosso, M., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
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Best Local Similarity 78.9%;
Matches 15; Conservative (
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Unpublished (1997)
                                                                        transformed lines
Unpublished
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; Core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 60)

3 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Ueske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

L Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
Fax: 858 558 6379
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agazose gel electrophoresis. Vector DNA was prepared from a derivative of pWD12 (gi[4732114]gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheard, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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NA insertion lines Arabidopsis
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/clone="SALK 095643"
/clone="SALK 095643"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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/wol_type="genomic DNA"
/strain="Columbia 0"
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095643 Arabidopsis thaliana TDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 92.3%
Local Similarity 92.3%
Local Similarity 92.3%
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 49)
S Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
  /strain="Columbia 0"
/db_xref="taxon:3702"
/dclone="XALK 131965.28.05.n"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="FCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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1M0547D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0547D09 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Insert Length: 10000 Std Error: 0.00
Plate: 0547 row: D column: 09
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Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers

    .49
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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/clone="UUGC1M0547D09"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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Fax: 801 585 7177
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84112, USA
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CB911682 79 bp mRNA linear EST 25-APR-2003 VVD134E08 373255 An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera CBNA clone VVD134E08 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="VVD134E08"
/tissue_type="berries"
/tissue_type="mixed, % 9, 11, 13, 15, 16 weeks daf"
/dev stage="mixed, % 9, 11, 13, 15, 16 weeks daf"
/dev stage="mixed, % 9, 11, 13, 15, 16 weeks daf"
/dev stage="mixed, % 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
ECORI; Site_2: XhoI"
                                                                                               Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9,392(6676):608-11)
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Epgermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 79)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                           Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                             /cell_type="embryonic stem cell"
/clone lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                       62.0%; Score 12.4; DB 29;
llarity 86.7%; Pred. No. 1.7e+05;
Conservative 0; Mismatches 2;
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                                                                                                                                                                                              1. .77
/organism="Mus musculus"
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PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 134 row: B column: 08
Seq primer: T3 20mer
High quality sequence stop: 79.
Location/Qualifiers
e
                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="129SV/EV"
/db_xref="taxon:10090"
/clone="0ST275491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cushman, J.C.
An expressed sequence tag databar
Vitis vinifers var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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/db_xref="taxon:29760"
                                                                                                                                                                          Location/Qualifiers
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Tel: 775-784-1918
Fax: 775-784-1650
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                                                                                                                                            Class: Gene Trap.
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 77)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Figgott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markeeich, D.,
Payne, R., Potter, D.G., Ojan, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Whal kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                CD903663 69 bp mRNA linear EST 14-JUL-2003 G356.110P16F010919 G356 Triticum aestivum cDNA clone G356110P16, mRNA sequence.
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                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence has been generated in the framework of the franch plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
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OST275491 Mus musculus 129SV/Ev Mus musculus genomic clone
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/tissue_type="grain (356 degrees per day after
pollination)"
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Pred. No. 1.7e+05;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
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Best Local Similarity 92.9%;
Matches 13; Conservative (
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37 ATCTATGTTTGGCT
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2M0003A19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0003A19 F, genomic survey sequence.
                                                                                                                                                                                                                                                 TAGA05P 24 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 6a05, forward sequence, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                Gaps
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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  Score 12.4; DB 14; Length 79;
Pred. No. 1.7e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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/clone="6a05"
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AZ774210.1 GI:12899399
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      62.0%;
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(bases 1 to 24)
                                                13; Conservative
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Matches 13; Conserv
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gril #191A1191BA12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent R. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reil, J., Kose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R., Tingey, A., von Dubse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male" | /sex="Male" | /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" | /clone lib="Mouse 10kb plasmid UUGCIM library" | /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jacksor Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 5td Error: 0
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Location/Qualifiers
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Best Local Similarity 82.4
Matches 14; Conservative
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Search completed: September 23, 2004, 16:43:34

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	September 23, 2004, 13:59:29; Search time 1263 Seconds (without alignments)
Title:	000.330 MILLION CELL UDGGCES/SEC US-10-798-923A-36
Perfect score:	
Seguence:	1 agtaacatctatgtttggtt 20

3470272 seqs, 21671516995 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 80

1774092

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries

99 ba: *
99 ba: *
99 ba: *
99 cov: *
90 cov: * GenEmbl:* Database :

Pred. No. is the number of results predicted by chance to have a

em_sy:* em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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.8 59.0 27 6 AXO08357 .8 59.0 27 6 BD218250 .8 59.0 29 6 180874 .8 59.0 31 6 AX792894 .8 59.0 31 6 BD002365 .8 59.0 32 6 E14590 .8 59.0 32 6 12666 .8 59.0 41 6 AX514674 .8 59.0 42 6 AX503648 .8 59.0 42 6 AX503648	ALIGNMENTS AR100077 Sequence 34 from patent US 6080546. AR100077.1 GI:12810525 Unknown. Unknown. Unknown. Unknown. Unknown. Unclassified. 1 (Dases 1 to 20) Antisense modulation of MEKKS expression Antisense modulation of MEKKS expression Patent: US 6080546-A 34 27-UNN-2000; Location/Qualifiers 1. 20 /organism="unknown"	Similari 5; Cons AGTAACA 	AJ591807 Arabidopsis thaliana T-DNA flanking sequence, left border, clone 529508. AJ591807 AJ591807 AJ591807.1 GI:37941431 left border; T-DNA flanking sequence. Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; poprmatophyta; Magnollophyta, edicots; rosids: entrosids 11: Massicales; Brassicaceae; Arabidopsis.	Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Chauvin,S., Echtold,N., Cruaud,C., DeRose,R., Pelletier,G., T-DNA integration into the Arabidopsis genome depends on seq of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002) 22363535 2 (bases I to 29) Balzergue,S. Direct Submission Submitted (23-OCT-2003) Balzergue S., UMRCV, INRA/CNRS, 2 rugaston Cremieux, 91057 Evry cedex, FRANCE
C 139 11. 140 11. 141 11. 142 11. 145 11. 147 11. 147 11. 147 11. 147 11. C 148 11. C 148 11. C 150 11. C	RESULT 1 ARIO077 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE REFERENCE AUTHORS FITTLE JOURNAL FEATURES	ORIGIN Query Match Best Local (Matches 1) Qy 1 Db 2	RESULT 2 AJ591807/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDILNE PUBMED REFERENCE AUTHORS TITLE JOURNAL
BD272920 Methods. AX026175 Sequence AJ587782 Arabidops E25013 Oligomucleo BD178885 NR10 spli 132311 Sequence AX225224 Sequence AX25224 Sequence AX25224 Sequence AX15449 Sequence AX15726 Sequence AX15726 Sequence	AJ59717 B Arabidops AJ529042 Arabidops AJ530578 Arabidops AJ01011018 Bacillus BD268125 Stabilize M64559 Mouse JH-Cd AX899169 Sequence BD034702 Sequence BX699149 Sequence AX699149 Sequence AX692811 Sequence AR028211 Sequence AR028215 Sequence AR028215 Sequence BD218407 Newcastle BD24508 Regions o I55027 Sequence 51 AJ520780 Arabidops AR29077 Sequence AX058573 Sequence	AL595268 Arabidops AF043755 Homo sapi AF043761 Homo sapi AF043762 Homo sapi AF043798 Homo sapi AF043756 Homo sapi AF043756 Homo sapi AF043755 Homo sapi AF043757 Homo sapi		AF043995 Acub sapi AF043985 Homo sapi AK043987 Homo sapi AX08487 Sequence BD218375 Newcastle AR436140 Sequence AX22775 Sequence AX22777 Sequence AX10579 Sequence AX105790 Sequence AX105790 Sequence AX10578 Antisence AX10578 Sequence AX1058 Sequence AX1058 Sequence AX1058 Sequence AX1058 Sequence AX1058 Sequence AX11658 Sequence AX11658 Sequence
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PAT 16-SEP-2000

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Friedrichs, U., Heppner, P., Ringeis, A., Lakner, M., Cullmann, G. and
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Patent: WO 0127612-A 54 19-APR-2001;
Connex Gesellschaft zur Optimierung von Forschung und Entwicklung
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                                                                                                                                                                                                                                                                                                                                                                                                          Detection of acid-resistant micro-organisms in a stool
Patent: WO 0026671-A 46 11-MAY-2000;
FRIEDRICHES ULRIKE (DE) ; CONNEX GMBH (DE) ; HEPPNER PETRA
RINGELS ACHIM (DE) ; LAKNER MERET (DE) ; CULLMANN GERHARD
REITER CHRISTIAN (DE)
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Best Local Similarity 88.2%; Pred. No. 7.5e+04;
Matches 15; Conservative 0; Mismatches 2;
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/organism="synthetic construct"

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    ^organism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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              Mismatches
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/db_xref="taxon:32630"
/note="kunstliche Sequenz"
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Sequence 46 from Patent W00026671.
AX025318
AX025318.1 GI:10187008
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Sequence 54 from Patent WO0127612.
AX113479
AX113479.1 GI:13939723
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AX113479
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PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante-info.infoblogen.fr).

Location/Qualifiers
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33 bp DNA linear PAT 17-JUL-2003
Novel method for detecting acid-resistant microorganisms in feces.
BD233882
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GOIN33/569, C07K16/12, G01N33/543, G01N33/577//C12P21/08, G01N33/
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1 (bases 1 to 33)
Reiter, C., Cullmann, G., Friedrichs, U., Heppner, P., Lakner, M. and
                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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CHRISTIAN REITER,GERHARD CULLMANN,ULRIKE FRIEDRICHS,PETRA PI
HEPPNER,
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Coganism="Arabidopsis thaliana"
/mol type="qenomic DNA"
/cultivar="Wassillewskija"
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Pred. No. 7.6e+04;
0; Mismatches 2;
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/note="T-DNA flanking sequence
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    .33
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    /db_xref="taxon:32630"

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JP 2002529705-A/22.
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artificial sequences.

It (bases 1 to 4)

Croteau, R.B. and Hefner, J.L.

Nucleic acids encoding taxus geranylgeranyl diphosphate synthase, and methods of two use
and methods of two use
and methods of use
by 200223077-A 8 10-SEP-2002;
WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
OS Artificial Sequence
by JP 2002252977-A/8

PP 27-CGT-1999 JP 2000581172

PR 05-NOV-1998 US 09/187050

PI RODNEY B CROTEAU, JERRY L HEFNER

PC CLISIS/09, CLIZN9/10, CLIZN9/10, (CLIZN15/00, PC)
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Patent: WO 0104324-A 3 18-JAN-2001;
Patent: WO 0104324-A 3 18-JAN-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
INSTITUT NATIONAL DE SOIENCES Appliquees de Toulouse (FR) ; Centre Institut National De La Recherche Scientifique (FR)
Location/Qualifiers
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                             BD241774 11-JUL-2003 Nucleic acids encoding taxus geranylgeranyl diphosphate synthase, and methods of use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium butyricum
Clostridium butyricum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC Description of Artificial Sequence:PCR primer CC for synthesizing Tr295 truncation product FH Key Location/Qualifiers
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Method for preparing 1,3-propanediol by a recombinant
micro-organism in the absence of coenzyme bl2 or one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 13.6; DB 6; Length 28;
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69.0%; Score 13.8; DB 6;
Best Local Similarity 88.2%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 2;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 3 from Patent W00104324
AX074559 AX074559.1 GI:12710662
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JP 2002529077-A/8.
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                                                                                                                         PAT 01-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parent: EP 1336850-A 54 20-AUG-2003;
Connex Gesellschaft zur Optimierung von Forschung und Ent wicklung
                                                                                                                                                                                                                                                                                                                                            Improved method for the detection of acid resistant microorganisms
                                                                                                                                                                                                                                                                                                                                                                   Patent: WO 0127613-A 54 19-APR-2001;
Connex Gesellschaft zur Optimierung von Forschung und Entwicklung
(DE)
                                                                                                                                                                                                                                                                                                    Reiter, C., Cullmann, G., Heppner, P., Ringeis, A., Mueller, H. and Haindl, E.
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    .33
    ^organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

    .33
forganism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="CDR"

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Sequence 54 from Patent EP1336850.
AX816281
AX816281.1 GI:39646788
                                                                                                                              AX113614 33 bp
Sequence 54 from Patent WO0127613.
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      AACATTAATGTTTGGTT 29
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VERSION KEYWORDS

PCR primer

Gaps .; 0 PAT 29-SEP-1999

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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATH521905 52 bp DNA linear PLN 29-MAR-2003
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Alavin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
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                                                                                                                                     Length 73;
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Bllis,N.A., German,J. and Groden,J.
Nucleic acids of the bloom's syndrome gene
Patent: US 5824501-A 14 20-OCT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.2; DB 6;
Pred. No. 1.5e+05;
                                                                                                                                   Query Match 68.0%; Score 13.6; DB 6; Best Local Similarity 80.0%; Pred. No. 8.3e+04; Matches 16; Conservative 0; Mismatches 4;
                     1. .73
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                DNA
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Sequence 14 from patent US 5824501.
AR049025
AR049025.1 GI:6005064
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/wol_type="unassigned DNA"
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
   Location/Qualifiers
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AJ521905
AJ521905.1 GI:26790141
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Balzergue, S.
Direct Submission
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PC C12N15/09,C12N1/19,C12N9/16//(C12N1/19,C12R1:645),(C12N1/19,
PC C12R1:78),
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RAINER MUBLLER, JOHANN PETER THALHOFER, FRANK GEIPEL, WERNER
                     Gaps
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synthetic construct
artificial sequences.

I (bases I to 73)
Mueller.R., Thalhofer.J.P., Geipel,F., Hoelke,W., Glaser,S.,
Eckstein,H., Kirschbaum,T. and Riebel,B.B.N.
Expression of alkaline phosphatase in yeast
Patent: JP 2002252269-A 26 10-SEP-2002;
F HOFFMANN IA ROCHE AG
OS Artificial Sequence
PN JP 2002253269-A/26
                                                                                                                                                                                                                                                                                                                                                                Glaser, S.,
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Expression of alkaline phosphatase in yeast
Patent: EP 1176205-A 27 30-JAN-2002;
Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG
Location/Qualifiers

    .73
/organism='Artificial Sequence'.

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BD175616
Best Local Similarity 80.0%; Pred. No. 9.5e+04; Matches 16; Conservative ' 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1...73
/organism="synthetic construct"
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/db_xref="traxon:32630"
/noTe="Artificial"
                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                        AX356671 73 bp
Sequence 27 from Patent EP1176205.
AX356671
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25-JUL-2000 DE 10036491
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                                                                                          26 AATAACATTTTTGTTTGTTT 7
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AX356671/c
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BD175616/c
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             the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
 plants from INRA (Versailles). The DNA fragment(s) resulting from
                                                                                                                                                                    1. .52

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Wassillewskija"

/db_xref="taxon:3702"

/clone="280G09"

/clone="1b="Arabidopsis thaliana T-DNA insertion lines"
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Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                    66.0%; Score 13.2; DB 8; Length 52; 83.3%; Pred. No. 1.3e+05;
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                     /note="T-DNA flanking sequence
left border"
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/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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1 Similarity 83.3%;
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Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
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AX180638
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synthetic construct
artificial sequences.
1 (bases 1 to 34)
Chen,P., Kan,C.C., Luo,C., Margosiak,S., OGconnor,P., Russell,A.T.,
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Tempczyk-Russel, A., Nguyen, B., Sarup, J.C., Gaur, S., Anderson, M.B.,
Dengy, Y.L., Lundgrent, K. and Register, J.
Catalytic domain of the human effector cell cycle checkpoint
protein kinase, chkl, materials and methods for identification of
inhibitors theroe,
Patent: EP 1096014-A 3 02-MAY-2001;
Agouron Pharmaceuticals, Inc. (US)
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Scalyye domain of human effector cell cycle check point protein kinase Chkl, and substance for identifying the inhibitor and identification method.

BD014871. GI:22555678

JP 2001161387-A/2.
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Osbourn, A.E., Haralampidis, K. and Bryan, G.T.
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87.5%; Pred. No. 2.2e+05;
iive 0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="PCR primer"
                                                                                                                                 /organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/nofe="primer"
              Plant gene
Plant gene
Patent: WO 0146391-A 216 28-JUN-2001;
Plant Bioscience Limited (GB)
Location/Qualifiers
1. 30
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Sequence 3 from Patent EP1096014.
AX136051
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synthetic construct
artificial sequences.
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PAT 12-JUN-2003
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0138566.A 475 31-MAY-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                           1 (bases 1 to 47)
Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 1887 25-MAR-2003;
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64.0%; Score 12.8; DB 6;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2;
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                                                                  AR290152 47 bp DN Sequence 1887 from patent US 6537751.
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Sequence 475 from Patent W00138586.
AX165280
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="unknown"
/mol_type="genomic_DNA"
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                                                                                                                                                                                                                                         Unclassified.
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AX008365/c
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Nguyen, B., Sarup, J.C., Gaur, S., Anderson, M.B., Deng, Y.L., Lundgren, K. and Register, J. Catalyst domain of human effector cell cycle check point protein kinase Chkl., and substance for identifying the inhibitor and identification method identification method AGOURON PHARMACEUTICALS INC OS Artificial Sequence PN JP 2001161387-A/2 PD 19-JUN-2001 PP 01-NOV-2000 JP 2000335268 PR 01-NOV-2000 JP 2000335268 PR 01-NOV-2000 JP 2000335268 PR 01-NOV-2000 JP 200035268 PR 01-NOV-20
                                                                                                                                                                                                                                                                                                                           O'CONNOR,
PI ANNA TEMPCZYK RUSSELL, BINH NGYYEN, JAY CHAND SARUP, SMITA GAUR,
PI MARK BRIAN ANDERSON, YA LI DENG, KAREN LUNDGREN, JAMES REGISTER
PC CIZNIS/09, CO7K19/00, CIZNI/21, CIZNS/10, CIZNI/00, CIZNS/12, CIZN9/
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Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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(C12N5/00,C12R1:91)
Description of Artificial Sequence: PCR primer FH
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism='Artificial Sequence'
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Seguence 1712 from Patent W002053728.
AX484412
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/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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AX48412/C
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Best Local Similarity 78.9
Matches 15; Conservative
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Roberts, C.J.
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AR194187/c
LOCUS
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AR147539/c
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AR142867/c
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Patent: WO 9966045-A 17 23-DEC-1999;
GIELKWAS ARNOUD LEDNARD JOSEF (NL); KOCH GUUS (NL); LEEUW OLAV SVEN
DE (NL); PEETIERS BENNARDUS PETRUS HUBER (NL); STICHTING DIENST
LANDBOUWKUNDI (NL)
Location/Qualifiers
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Newcastle disease virus infectious clones, vaccines and diagnostic
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19-UUN-1998 EP 98202054.7
BERNARDUS PERTRUS HUBERTUS PEETERS, OLAV SVEN
LEEUW, GUUS KOCH,
ARNOUD LEONARD JOSEF GIELKENS
C12N15/09, A61K39/17, A61K48/00, A61P31/12, C12N7/00, C12Q1/70, PC
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BD218258.1 construct
synthetic construct
artificial sequences.
1 (bases I to SB)
Peters, B.P.H., ineeuw, O.S.D., Koch, G. and Gielkens, A.L.J.
Newcastle disease virus infectious clones, vaccines and diagnostic
                                                                      Gielkens, A.L., Koch, G., De Leeuw, O. and Peeters, B.P.
Newcastle disease virus infectious clones, vaccines and diagnostic
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OS ARLIficial Sequence
OS ARLIficial Sequence
PN UP 2002518012-A/17
PD 25-UUN-2002
PF 17-UUN-1999 UP 200554854
PR 19-UUN-1999 UP 200554854
PR ARNOUD LEONARD JOSEF GIELKENS
PC C12N15/00
C12N15/00
CC /note='Primer BGLSF2'
CC Description of Artificial Sequence: primer
FH KEY
FT Primer_bind (1). (58).
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64.0%; Score 12.8; DB 6; Length 58;
Best Local Similarity 87.5%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
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Key

Location/Qualifiers

Location/Qualifiers
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/organism="synthetic construct"
/nol_type="unassigned DNA"
/db_xref="taxon:32630"
1. .58
/note="'Primer BGL5F2'
primer"
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                         synthetic construct artificial sequences.
          synthetic construct
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Matches 14; Conservative
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                                                                                                                                                                 Essential genes of yeast as targets for antifungal agents, herbicides, insecticides and anti-proliferative drugs Patent: US 6221597-A 53 24-APR-2001; Location/Qualifiers
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64.0%; Score 12.8; DB 6; Length 74;

Best Local Similarity 87.5%; Pred. No. 2e+05;

Matches 14; Conservative 0; Mismatches 2; Indels
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1 (bases 1 to 24)
O'DWYer,K.W. Warren,R. and Perry,C. Sec A2 from Streptococcus pneumoniae Patent: US 6204019-A 5 20-WAR-2001;
Location/Qualifiers
74 bp
Sequence 53 from patent US 6221597.
AR147539
AR147539.1 GI:15111342
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 5 from patent US 6348342.
AR194187.1 GI:20240779
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AR142867
AR142867.1 GI:15104153
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/organism="unknown"
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Synthetic oligo 50.
A35752
A35752.1 GI:1927123
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artificial sequences.
1 (bases 1 to 35)
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Best Local Similarity 78.9
Matches 15; Conservative
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Best Local Similarity 7
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Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
Miller,A. and North,M.
Asthma related genes
Patent: US 6087485-A 223 11-UUL-2000;
Location/Qualifiers
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unidentified
unidentified
unclassified.
E 1 (bases 1 to 27)
S Wilson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
Miller,A. and North,M.
Asthma-associated gene
L Patent: JP 2002500895-A 219 15-JAN-2002;
AXYS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002500895-A/219
PP 11-JAN-2002
PP 21-JAN-2002
PP 21-JAN-2002
PP 21-JAN-2004
PP 2004500895-A/219
PP 31-JAN-2004
PP 31-JAN-2007
PP 31-JAN-20
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Pred. No. 2.9e+05;
0; Mismatches 4; Indels
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Pred. No. 2.8e+05;
0; Mismatches 4; Indels
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1 (bases 1 to 24)
O'Dwyer,K.M., Warren,R. and Perry,C.
Compounds
Patent: US 6348342-A 5 19-FEB-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 223 from patent US 6087485. AR103699
                                                                                                       1. .24
/organism="unknown"
/mol_type="unassigned DNA"
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JP 2002500895-A/219.
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BD129929
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Best Local Similarity 78.9%;
Matches 15; Conservative
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Best Local S:
Matches 15,
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AR103699/c
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BD129929/c
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PAT 06-FEB-1997
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                                                                     /organism='Unidentified'. Location/Qualifiers
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                                     Location/Qualifiers
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Higaki,J.N., Tischer,E.G., Cordell,B. and
Production of homogeneous truncated CNTF
Patent: US 5593857-A 3 14-JAN-1997;
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Patent: WO 9308273-A 50 29-APR-1993;
Location/Qualifiers
1, .35
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 3 from patent US 5593857.
I33654
                                                                                                           1. .27
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Topology: Linear;
Asthma-associated
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RESULT 30

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ACCESSION VERSION KEYWORDS REFERENCE

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PAT 06-JUL-2002
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                                                                          Unclassified.

1 (bases 1 to 36)

1 (bases 1 to 36)

Ballance, D.J., Courtney, M.G., Finnis, C.J.A. and Sleep, D.

Modulation of cellular proliferation with thymidine phosphorylase Patent: US 6290953-A 49 18-SEP-2001;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki,Y.
Method for base sequencing and biologically active nucleic acids
Patent: WO 0244195-A 15 06-JUN-2002;
RIKEN (JP)
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Stanley, C.John., Orum, H. and Jorgensen, M.
Nucleic acid analogs with a chelating functionality
Patent: US 6346378-A 11 12-FEB-2002;
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/mol_type="unassigned DNA"

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/organism="unknown"
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    .36
    /organism="unknown"
    /mol_type="unassigned DNA"

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AX453001
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AR168999
AR168999.1 GI:17906697
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AR184398/c
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AX453001/c
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1 (bases 1 to 35)

Ballance,D.J., Courtney,M.G., Finnis,C.J.A. and Sleep,D.

Modulation of cellular proliferation with thymidine phosphorylase
Patent: US 6290953-A 50 18-SEP-2001;

Location/Qualifiers
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PATENT: WO 9308273-A 49 29-APR-1993;
Location/Qualifiers
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63.0%; Score 12.6; DB 6; Length 36;
Best Local Similarity 78.9%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels
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 Score 12.6; DB 6; Length 35;
Pred. No. 2.7e+05;
0; Mismatches 4; Indels
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    .36
    forganism="synthetic construct"
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|db_xref="taxon:32630"

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DEFINITION Sequence 49 from patent US 6290953.
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/organism="unknown"
/mol_type="unassigned DNA"
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artificial sequences.
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Synthetic oligo 49.
A35751
A35751.1 GI:1927122
    Query Match 63.0%;
Best Local Similarity 78.9%;
Matches 15; Conservative (
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Best Local Similarity 78.9
Matches 15; Conservative
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RESULT 31 A35751/c

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PAT 17-JUL-2003
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24-SEP-1999 JP 2000572337
25-SEP-1998 US 60/101939
MICHAEL W LASSNER, ROBIN A EMIG, DIANE M RUEZINSKY, ALISON VAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC C12N15/09, A01H5/00, C12NS/10//C12N9/10, C12N15/00, C12N5/00 CC Description of Artificial Sequence: Synthetic Oligonucleotide FH Key
                                                                                                                              Gaps
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2712 Hessian fly genomic DNA Mayetiola destructor STS genomic,
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Mayetiola destructor
Eukaryota, Matazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Nematocera; Sciaroidea;
Cecidomyiidae; Mayetiola.
1 (bases I to 60)
Behura,S.K., Rider,S.D., Valicente,F.H. and Staurt,J.J.
Hessian fly STS markers
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synthetic construct
artificial sequences.
I (bases I to 60)
Lassner, M.W., Emig, R.A., Ruezinsky, D.M. and Eenennaam, A.V.
Novel plant acyltransferases
Patent: JP 2002525105-A 175 13-AUG-2002;
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0
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                     1. .59
/note="polymorphic AFLP marker EAC/MCTG-82"
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Location/Qualifiers
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                                                                                          Length
                                                                                                                                                                                                                                                                                   linear
                                                                                                                            Indels
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        /map="between G15-1 and EAC/MCTA-201"
                                                                                        Score 12.6; DB 11;
Pred. No. 2.5e+05;
0; Mismatches 4;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon.32630"
                                                                                                                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                          Novel plant acyltransferases.
BD224826
                                                                                                                                                        2 GTAACATCTATGTTTGGTT 20
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JP 2002525105-A/175
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JP 2002525105-A/175.
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BV079655
BV079655.1 GI:34787404
                                                                                       ch 63.0%;
1 Similarity 78.9%;
15; Conservative
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nes 15; Conserva
                                                                                        Query Match
Best Local Similarity
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BV079655/c
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BD224826
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Submitted (27-SEP-2001) Entomology, Purdue University, 1158 Smith
Hall, West Lafayette, IN 47907-1158, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                       Gaps
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Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;
Cecidomylidae; Mayetiola.
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Rider, S.D. Jr., Sun, W., Ratcliffe, R.H. and Stuart, J.J.
Chromosome landing near avirulence gene VH13 in the Hessian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mayetiola destructor chromosome X2 map between G15-1 and EAC/MCTA-201, sequence tagged site.
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                                                                 63.0%; Score 12.6; DB 6; Length 50; 78.9%; Pred. No. 2.6e+05; ive 0; Mismatches 4; Indels
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/mol_type="genomic DNA"
/dD_xref="taxon:39758"
/chromosome="X2"
                                                                                                                                                                                                                                                          55 bp DNA WO02053728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .55
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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Mayetiola destructor
/db_xref="taxon:32630"
/note="a spacer"
                                                                                                                                                                                                                                                     AX485769
Sequence 3069 from Patent
AX485769
                                                                                                                                   1 AGTAACATCTATGTTTGGT 19
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                                                                                                                                                            21 AGTGTCATCTATGTCGGGT 3
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                                                                Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
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2 (bases 1 to 59)
Stuart,J.J.
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Matches 15; Conservative
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SOURCE
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AF424885/c
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AX485769
LOCUS
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G06F15/40
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(bases 1 to 79)

Latif,F., Modi,W.S., Duh,F.M., Schmidt,L., Li,H., Geil,L., Modi,W.S., Duh,F.M., Rabbitts,P.H., Linehan,W.M. et,al. Molecular and genetic characterization and physical mapping of 11 new markers detecting multiallele restriction fragment length polymorphisms on the short arm of human chromosome 3 Hum. Genet. 90 (1-2), 17-22 (1992)
                                                                                                                                                                                                                                                                                                                        C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(bases I to 63)

Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.

Sequence tag and encoded human protein

Patent: JP 2001269182-A 30225 02-OCT-2001;
                                                                                                                                                                                                            Hemo sapiens (human)
JP 2001269182-A/30225
02-OCT-2001
24-FEB-2000 JP 2000118773
25-FEB-1999 US 60/122487
JEAN BADUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 General staff at the National Library of Medicine created this entry [NCBI gibbsq 117048] from the original journal article. This sequence comes from Fig. 2.
Map location: 3p26.
Location/Qualifiers
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D38745 {VNTR repeat element} [human, Genomic, 79 nt].
S47006
S47006.1 GI:258800
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Sequence tag and encoded human protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
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/db xref="taxon:9606"
1. 79
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/organism="Homo
               BD053979
BD053979.1 GI:22599585
JP 2001269182-A/30225.
Homo sapiens (human)
Homo sapiens
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/gene="D3S745"
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PC C12P2
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Best Local S
Matches 15
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ORGANISM
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PUBMED
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.6; DB 11; Length 60; Pred. No. 2.5e+05;
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Pred. No. 2.5e+05;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                               Department of Entomology
Purdue University
901 W State St., West Lafayette, IN 47907, USA
Primer A: None provided
Primer B: None provided
                                                                                                                                                                                                                                                                                                                                                                             /moi_type="genomic DNA"
/db_xref="taxon:39758"
/clone lib="Hessian fly genomic DNA"
<1. .>60
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each 2000m
0.1 units/ul
25 ul
                                                                                                                                                                                                                                                                                                                                                    .. .60
'organism="Mayetiola destructor"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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50 mM
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Total Vol:
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Best Local Similarity 78.9%;
Matches 15; Conservative
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KCl:
Tris-Cl:
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                                   Contact: Jeff Stuart
                                                                                                                                                                        Primer:
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      Unpublished (2003)
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                        Protocol:
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BD053979/c
LOCUS
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SOURCE
ORGANISM
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AX918446/c
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DRIGIN

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 42

AX241123 LOCUS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Direct Submission
Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91657 Evry cedex, FRANCE
CASTON TRAN (Versailles). The DNA fragment (8) resulting from
the PCR was performed on DNA from transformants of Arabidopsis thalians
plants from INRA (Versailles). The DNA fragment (6) resulting from
the PCR were directly sequence from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsqap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                        ATH531902 37 bp DNA linear PLN 29-MAR-2003 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                         Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
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                                                                                                                                                                                                                left border, T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.4; DB 8;
Pred. No. 3.4e+05;
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/note="T-DNA flanking sequence
left border"
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AJ531902.1 GI:26800162
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Staphylococcus aureus
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X59477.1 GI:46621
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Best Local Similarity 92.9
Matches 13; Conservative
20 CAGCTATGTTTGGT
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                                                            RESULT 44
ATH531902
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.
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Microsatellite markers from Triticum tauschii
Patent: EP 121707-A 461 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
Location/Qualifiers
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Gene disruption methodologies for drug target discovery
Patent: WO 0160975-A 361 23-AUG-2001;
Elitra Pharmaceuticals, Inc. (US)
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                                Score 12.6; DB 9; Length 79;
Pred. No. 2.4e+05;
0; Mismatches 4; Indels
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Pred. No. 2.4e+05;
0; Mismatches 4; Indels
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Pred. No. 3.7e+05;
0; Mismatches 1;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                 DNA
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/mol_type="unassigned DNA"
/db_xref="taxon:37682"
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Sequence 361 from Patent WO0160975.
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78.9%;
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synthetic construct
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1 Similarity 92.9%;
13; Conservative
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                                                                            Conservative
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Matches 15; Conserv
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RESULT 43 AX462717/c LOCUS

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KEYWORDS SOURCE ORGANISM

AUTHORS JOURNAL

FEATURES

REFERENCE

Matches

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Gaps

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Bacteria; Firmicutes; Bacillales; Staphylococcus.

Bacteria; Firmicutes; Bacillales; Staphylococcus.

Dyke K.G.H., Curnock, S.P., Golding, M. and Noble, W.C.
Cloning of the gene conferring resistance to mupirocin in Staphylococcus aureus aureus aureus aureus aureus aureus aureus area forganism="Staphylococcus aureus"

Location(Qualifiers 1.7, 195-198 (1991)

Gorganism="Staphylococcus aureus"

Mod. type="Staphylococcus aureus"

Amol. type="Mod. type="Staphylococcus aureus"

Aplasmid="Pox301"

Aplasmid="Pox301"

Aplasmid="Pox301"

Aplasmid="Mod. tesistence gene"

Agene="mupirocin resistence gene"

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Search completed: September 23, 2004, 16:21:00 Job time : 1274 secs

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